

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:34:17 ; Search time 114 Seconds
(without alignments)
588.442 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668

Sequence: 1 MANKMPQITSTANKIWS.....NAGLGFLDPTAAIVSSDITTA 131

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668	100.0	131	2 Q9AZ42	Q9az42 bacterioph
2	80	12.0	194	1 LPPK MYCLE	Q49803 mycobacteri
3	79	11.8	918	1 IL6B HUMAN	P40189 homo sapien
4	78.5	11.8	559	2 Q26645	Q26645 strongyloce
5	78.5	11.8	667	2 Q6LOE7	Q6lce7 photobacter
6	78	11.7	305	2 Q9RT24	Q9rt24 deinococcus
7	78	11.7	6146	2 Q93HJ5	Q93hj5 streptomyce
8	77.5	11.6	1454	2 Q8ENZ2	Q8enz2 oceanobacill
9	77	11.5	373	2 Q74KV6	Q74kv6 lactobacill
10	77	11.5	1088	2 Q6ZUM6	Q6zum6 homo sapien
11	76.5	11.5	457	2 Q6CJF9	Q6cjf9 yarrowia li
12	76.5	11.5	546	1 CH60_CHRVI	P31293 chromatium
13	76	11.4	436	2 Q74BT9	Q74bt9 geobacter s
14	76	11.4	538	2 Q7WSS8	Q7ws88 pseudomonas
15	76	11.4	540	2 Q7SG34	Q7sg34 neurospora
16	75.5	11.3	519	1 ACHG BOVIN	P13536 bos taurus
17	75.5	11.3	1174	2 Q8MPR0	Q8mpr0 crassostrea
18	75	11.2	386	2 Q8P9T4	Q8p9t4 xanthomonas
19	75	11.2	711	2 Q6MKR4	Q6mkra bdellovibri
20	74.5	11.2	1333	2 Q6L3N8	Q6l3n8 solanum dem
21	74	11.1	620	2 Q12623	Q12623 humicola gr
22	74	11.1	657	1 BTK CHICK	Q8jbe4 gallus gall
23	74	11.1	713	2 Q8EV63	Q8ev63 mycoplasma
24	74	11.1	988	2 Q871D1	Q871d1 vibrio para
25	74	11.1	1693	2 Q7RLG9	Q7rlg9 plasmodium
26	74	11.1	2799	1 G112 HUMAN	Q8irf6 homo sapien
27	73.5	11.0	213	2 Q50402	Q50402 mycobacteri
28	73.5	11.0	291	2 Q9SBF9	Q9sbf9 arabidopsis
29	73.5	11.0	236	2 Q7TWL6	Q7twl6 mycobacteri
30	73.5	11.0	830	2 Q9U3V0	Q9u3v0 toxoplasma
31	73.5	11.0	831	2 Q92D26	Q92d26 listeria in

32 73.5 11.0 3550 2 Q66GT4 Q66gt4 rattus norv
33 73.5 11.0 7048 2 Q6D739 Q6d739 erwinia car
34 73 10.9 214 2 Q9SXH1 Q9sxh1 physcomitre
35 73 10.9 547 2 Q8Y5Y8 Q8y5y8 listeria mo
36 72 10.8 273 1 FWDC METJA Q8571 methanococc
37 72 10.8 517 2 Q8FBB3 Q8fbb3 escherichia
38 72 10.8 524 2 Q42147 Q42147 xenopus lae
39 72 10.8 524 2 Q8AVN9 Q8avn9 xenopus lae
40 72 10.8 680 2 Q9N9G7 Q9n9g7 phallusia m
41 72 10.8 1084 2 Q6BGK7 Q6bgk7 paramecium
42 72 10.8 4032 2 Q7WTF3 Q7wtf3 streptomyce
43 71.5 10.7 173 2 Q9AI69 Q9aig9 helicobacte
44 71.5 10.7 619 2 Q8H8S5 Q8h8s5 oryza sativ
45 71.5 10.7 1199 1 TTL4_HUMAN Q14679 homo sapien

ALIGNMENTS

RESULT 1
Q9AZ42 PRELIMINARY; PRT; 131 AA.
ID Q9AZ42
AC Q9AZ42;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Coat protein.
OS Bacteriophage AP205.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=154784;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22024855; PubMed=12029168;
RA Klovins J., Overbeek G.P., van den Worm S.H., Ackermann H.W.,
RA van Duijn J.,
RT "Nucleotide sequence of a ssRNA phage from Acinetobacter: kinship to
RT coliphages.";
RL J. Gen. Virol. 83:1523-1533(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Klovins J.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334111; AAK20390.1; -;
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; P:Structural molecule activity; IEA.
KW Coat protein.
SQ SEQUENCE 131 AA; 14009 MW; FB4ECBCBB8E12982 CRC64;

Query Match 100.0%; Score 668; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 8.1e-60;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQVKVGIARLNNSGQVSVYKRPAP 60
DB 1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQVKVGIARLNNSGQVSVYKRPAP 60
QY 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAEWETHKRNVDTLFASGNAGLGFLDP 120
DB 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAEWETHKRNVDTLFASGNAGLGFLDP 120
QY 121 TAAIVSSDITTA 131
DB 121 TAAIVSSDITTA 131

RESULT 2
LPPK MYCLE STANDARD; PRT; 194 AA.
ID LPPK MYCLE
AC Q49803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)

```
DE Putative lipoprotein lppk precursor.
GN Name=lppk; OrderedLocName=ML1315;
GN ORFNames=MLCB2533.llc, B2126_F3_115;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churchev C.M., Harris D.E.,
RA Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrall B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Potential).
CC -1- SIMILARITY: Belongs to the MTB12 family.
CC
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CC
CC EMBL; U00017; AAA17217.1; -.
DR EMBL; AL035310; CAA22925.1; -.
DR EMBL; AL583921; CAC31696.1; -.
DR PIR; S72877; S72877.
DR Leproma; ML1315; -.
DR InterPro; IPR000437; Prok lipoprot_S.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
FT SIGNAL 1 26 Potential.
FT CHAIN 27 194 Putative lipoprotein lppk.
FT LIPID 27 27 S-diacylglycerol cysteine (By
similarity).
FT LIPID 27 27 N-palmitoyl cysteine (By similarity).
SQ SEQUENCE 194 AA; 20460 MW; E375262FC3218A86 CRC64;
Query Match 12.0%; Score 80; DB 1; Length 194;
Best Local Similarity 25.0%; Pred. No. 6.4;
Matches 30; Conservative 10; Mismatches 26; Indels 54; Gaps 6;
Qy 8 PITSTANKIYWS--DPTSLSTFTPSASLLRQVKVGIAGLNNVSGQYVSVYK-----RPAP 60
Db 110 PMTFTANNIAWSNKNPSDLATIS-----VNIAQTNN-----SVFSFPMETFPF 154
Qy 61 KPECCADACVMPNENOSIRTVISGSAENLATLKAETHKRVNVDTLFASGNAGLGFLDP 120
Db 155 PPQ-----QSWQLSKRTADMLLEFGNSG-GLTNP 182
RESULT 3
IL6B_HUMAN
ID IL6B_HUMAN STANDARD; PRT; 918 AA.
AC P40189; Q9UQ41;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
```

25-OCT-2004 (Rel. 45, Last annotation update)
Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin M
6 signal transducer) (Membrane glycoprotein 130) (gp130) (Oncostatin M
receptor) (CDW130) (CD130 antigen).
GN Name=IL6ST;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Myeloma, and Placenta;
RL MEDLINE=91084844; PubMed=2261637; DOI=10.1016/0092-8674(90)90411-7;
RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
gp130.";
RL Cell 63:1149-1157(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX TISSUE=Synovium;
RL MEDLINE=20341529; PubMed=10880057;
RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
RA Murakami M., Nakao K.;
RT "Cloning of novel soluble gp130 and detection of its neutralizing
autoantibodies in rheumatoid arthritis.";
RL J. Clin. Invest. 106:137-144(2000).
RN [3]
RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=21269388; PubMed=9501088; DOI=10.1074/jbc.M009979200;
RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
RT "Determination of the disulfide structure and N-glycosylation sites of
the extracellular domain of the human signal transducer gp130.";
RL J. Biol. Chem. 276:8244-8253(2001).
RN [4]
RP "Crystal structure of a cytokine-binding region of gp130.";
RX Bravo J., Staunton D., Heath J.K., Jones E.Y.;
RT "Crystal structure of a cytokine-binding region of gp130.";
RL EMBL J. 17:1665-1674(1998).
CC -1- FUNCTION: Signal-transducing molecule. The receptor systems for
IL6, LIF, OSM, CNTF, IL11 and CT1 can utilize gp130 for initiating
signal transduction. Binds to IL6/IL6R (alpha chain) complex,
resulting in the formation of high-affinity IL6 binding sites, and
transduces the signal. Does not bind IL6. May have a role in
embryonic development (By similarity).
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=P40189-1; Sequence=Displayed;
Name=2; Synonyms=GP130-RAPS;
IsoId=P40189-2; Sequence=VSP_001684; VSP_001685;
TISSUE SPECIFICITY: Found in all the tissues and cell lines
examined. Expression not restricted to IL-6 responsive cells.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
activation.
CC -1- DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis
(RA) but it is not specific to patients with RA.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 2.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
CC
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DR GO: 0005634; C:nucleus; IEA.
DR GO: 0003700; F:transcription factor activity; IEA.
DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000418; Ets.
DR InterPro: IPR002341; HSF ETS.
DR InterPro: IPR010993; SAM_homology.
DR InterPro: IPR003118; SAM_PNT.
DR Pfam: PF001178; Ets; 1.
DR Pfam: PF02198; SAM_PNT; 1.
DR PRINTS: PR00454; ETSDOMAIN.
DR SMART: SM00413; ETS; 1.
DR SMART: SM00251; SAM_PNT; 1.
DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
DR PROSITE: PS0061; ETS_DOMAIN_3; 1.
DR DNA-binding; Nuclear protein.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 559 AA; 62052 MW; 509EAFCT7ACBD21 CRC64;

Query Match 11.8%; Score 78.5; DB 2; Length 559;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 40; Conservative 27; Mismatches 51; Indels 39; Gaps 7;

QY 2 ANKPMQ---PITSTANKIVWSDP-----TRLSTTFASLLRQVKVGIAGLNNVSGQYVS 53
DB 208 ANVPAOSSSSSTSSSSSTASPPVSVTTTSTTTTSSSSSLSQIK-----LENVSSGYN 262
QY 54 V-----YKRP-----APKEGACADACVIMPENQSIQRTVIGSSAENLA 91
DB 263 TTSCMPLRDLFLAQGSVDQVAPVSAPOCSGFSFG---MYQVSESLQTINEFNAEDIL 319
QY 92 TLKAEWETHKRNVDTLFASGNAGLGLFDL-PTAAIVSS 127
DB 320 NIKQEDTSGSSDYVLSLESSPNSQHFLETPTELYNN 356

RESULT 5
Q6LOE7 PRELIMINARY; PRT; 667 AA.
AC Q6LOE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical methyl-accepting chemotaxis protein.
GN Names:PSPT0323; OrderedLocusNames:PBPA2077;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Camata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR178669; CAC20479.1; -
DR GO: 0016020; C:membrane; IEA.
DR GO: 0004871; F:signal transducer activity; IEA.
DR GO: 0006935; P:chemotaxis; IEA.
DR GO: 0007165; P:signal transduction; IEA.
DR InterPro: IPR004089; Chmtaxis trans.
DR InterPro: IPR003660; His_kin_HAMP.
DR InterPro: IPR000727; T_SNARE.
DR Pfam: PF00672; HAMP; 1.
DR Pfam: PF00015; MCPsignal; 1.
DR SMART: SM00304; HAMP; 1.
DR SMART: SM00283; MA; 1.
DR PROSITE: PS0111; CHEMOTAXIS_TRANSDUC_2; 1.
DR PROSITE: PS00885; HAMP; 1.
DR PROSITE: PS0192; T_SNARE; 1.
KW Complete proteome; Hypothetical protein.
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SQ SEQUENCE 667 AA; 73612 MW; B1D05DE9D060532C CRC64;

Query Match 11.8%; Score 78.5; DB 2; Length 667;
Best Local Similarity 24.8%; Pred. No. 41;
Matches 35; Conservative 22; Mismatches 53; Indels 31; Gaps 6;

QY 2 ANKPMQPIIT-----STANKIVWSDPTRLSTTFASLLRQVKVGIAGLNNVSGQYVS 55
DB 420 ANETMQVITAINEMASTABEVARTNTTSTVSHNATVAADQSK---AAVNKATDSVALLM 476
QY 56 KRPAPKEGACADACVIMPENQSIQRTVIS-----GSAENLATLKAWEETHKRNVDTLFAS 110
DB 477 TQIETASENTE-----MSNETQKISTVLNVIRDIASQTNLLALNAIEAAR-----A 524
QY 111 GNAGLGLDPTAAIVSSDTTA 131
DB 525 GDQGRGF-----AVVADEVRA 540

RESULT 6
Q9RT24 PRELIMINARY; PRT; 305 AA.
AC Q9RT24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Malonyl CoA-acyl carrier protein transacylase.
GN OrderedLocusNames:DR1945;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Uitterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577 (1999).
DR EMBL; AE002033; AAFL1497.1; -.
DR FIR; A75334; A75334.
DR HSSP; P25715; IMLA.
DR TIGR; DR1945; -.
DR GO: 0016740; F:transferase activity; IEA.
DR GO: 0004314; F:[acyl-carrier protein] S-malonyltransferase. .; IEA.
DR GO: 0006633; P:fatty acid biosynthesis; IEA.
DR GO: 0008152; P:metabolism; IEA.
DR InterPro: IPR001227; Ac_transferase.
DR InterPro: IPR004410; Fabb.
DR Pfam: PF00698; Acyl_transf_1; 1.
DR TIGRfams; TIGR00128; fabb; 1.
KW Complete proteome.
SQ SEQUENCE 305 AA; 31284 MW; 0564188B9PA35B9F CRC64;

Query Match 11.7%; Score 78; DB 2; Length 305;
Best Local Similarity 28.9%; Pred. No. 18;
Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;

QY 13 ANKIVWSDPTRLSTTFASLLRQVKVGIAGLNNVSGQYVSVKRPAPKEGC-ADACVI 71
DB 103 AGVLTLEDALRL--TRKRGELMQQAVPEGVGSAVMGD-----PAVVAEVCQAQGVV 154
QY 72 MP--NQNSIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGLDPTAAIVSSDTT 130
DB 155 QPANFNAPTQTVISGEKAAVDAASAEKLTGKALPLKVSAPFCALMRPAAEGLSAELH 214
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QY 131 A 131
Db 215 A 215

RESULT 7
Q93HJ5 PRELIMINARY; PRT; 6146 AA.
ID Q93HJ5
AC Q93HJ5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Modular polyketide synthase.
GN Namesolmal; OrderedLocusNames=SAV2899;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RL Nat. Biotechnol. 21:526-531(2003).
DR ENBL; AB070940; BAB69192.1; -.
DR ENBL; AP005033; BAC70610.1; -.
DR HSSP; P66202; IPQW.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0003960; F:NADPH:quinone reductase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006333; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR001227; Ac transferase.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR000794; ketoacyl_synth.
DR InterPro; IPR002029; Pept_S8_S53.
DR InterPro; IPR006163; Phosphateth_bind.
DR InterPro; IPR006162; Ppantne_S.
DR InterPro; IPR002364; OOR_zeta_crystal.
DR Pfam; PF00698; Acyl_transf_1; 4.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR Pfam; PF00109; ketoacyl-synt_C; 4.
DR Pfam; PF02801; ketoacyl-synt_C; 4.
DR Pfam; PF00550; PP-binding; 4.
DR PROSITE; PS00075; ACP_DOMAIN; 4.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 3.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 3.
DR PROSITE; PS01162; QOR_ZETA_CRYSTAL; 1.
DR PROSITE; PS01136; SUBTILASE_ASP; UNKNOWN 1.
KW Complete proteome; Phosphopantetheine; Transferase.
SQ SEQUENCE 6146 AA; 637476 MW; 1D56F1108D459D00 CRC64;

Query Match 11.7%; Score 78; DB 2; Length 6146;

Best Local Similarity 36.1%; Pred. No. 7.2e+02;
Matches 35; Conservative 10; Mismatches 42; Indels 10; Gaps 4;

QY 24 LSTFTSASLLRQVKVIGIAELNNVSGQYVYKRPAPKEGCA----DACVIMPENQSI 79
Db 3100 LSLEDGAALVTLRSRL-IABELSGHGMVSVSPADTAERIARWNGGICVAANNRRS- 3157

QY 80 RTVISGSAENLATLKAWE---THKRVDTLPAAGNA 113
Db 3158 -TVSGEPEALAEALAECEAGVRARRIPVDVASHSA 3193

RESULT 8
Q8ENZ2 PRELIMINARY; PRT; 1454 AA.
ID Q8ENZ2
AC Q8ENZ2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bacillopeptidase F (EC 3.4.21.-).
GN OrderedLocusNames=OB2331;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831;
RX MEDLINE=22202767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT ridge and its unexpected adaptive capabilities to extreme
RT environments."
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -I- SIMILARITY: Belongs to peptidase family S8.
DR ENBL; AP004600; BAC14287.1; -.
DR HSSP; Q99405; IMPT.
DR MEROPS; S08.017; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR009020; Prot_inh_propept.
DR InterPro; IPR010259; Prot_inh_S8A.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF05922; Subtilisin_N; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Complete proteome; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 1454 AA; 155494 MW; 9223ADF205D7FF7F CRC64;

Query Match 11.6%; Score 77.5; DB 2; Length 1454;
Best Local Similarity 29.4%; Pred. No. 1.4e+02;
Matches 25; Conservative 15; Mismatches 42; Indels 3; Gaps 1;

QY 47 VSGQYVYKRPAPKEGCAACVIMPENQSI RTVISGSAENLATLKAWE THKRVDTLPAAGNA 106
Db 165 VNGIATVATKVAEKVATFAEVEKILPNETRELYTTVDKDAE---TPKSDVANVENVER 221

QY 107 LPASGNAGLGFLDPTAAIVSSDTTA 131
Db 222 VGAPATWNNMGFDGSGVVVASIDTGA 246

RESULT 9
Q74KV6 PRELIMINARY; PRT; 373 AA.
ID Q74KV6
AC Q74KV6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DNA polymerase IV.
GN OrderedLocusNames=LJ0471;

```



```
RL J. Bacteriol. 186:2757-2765(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SYK-6;
RX MEDLINE=22188250; PubMed=12200295;
RX DOI=10.1128/AEM.68.9.4416-4424.2002;
RA Masai E., Harada K., Peng X., Kitayama H., Katayama Y., Fukuda M.;
RT "Cloning and characterization of the ferulic acid catabolic genes of
RT Spingomonas paucimobilis SYK-6.";
RL Appl. Environ. Microbiol. 68:4416-4424(2002).
CC -1- SIMILARITY: Belongs to the TPP enzyme family.
DR EMBL; AB110975; BAC79260.1; -.
DR HSP; P07342; IUSC.
DR InterPro; IPR00399; Pyruvate decarb.
DR Pfam; PF00205; TPP_enzyme_M; 1.
DR Pfam; PF02776; TPP_enzyme_N; 1.
DR PROSITE; PS00187; TPP_ENZYMES; 1.
KW Hypothetical protein.
SQ SEQUENCE 538 AA; 56498 MW; EFFE92E0EEF305CB CRC64;
  Query Match 11.4%; Score 76; DB 2; Length 538;
  Best Local Similarity 27.9%; Pred. No. 57;
  Matches 43; Conservative 15; Mismatches 50; Indels 46; Gaps 9;
QY 5 PMQPTSTANKIIVSDPTRLSTTFSASLLRQKVKVIGIAELNNVSGQY--VSVYKRPAPKP 62
Db 298 PYVPEGASLIQIV-DDPS-----VAARTPVGTAIIGNVADAIARLSAATSAP-P 345
QY 63 EGCADACVIMPNENQSIPTVIGSA-----ENLATLKA-----WETH- 100
Db 346 RAVPDAALPAPN-----VVGSGTAIEEALLMQQLATLRPKGIIEEAPSTRGPMHDF 399
QY 101 -KRNVDTLFASGNAGLGFLDPT---AAIVSSDIT 130
Db 400 PIRLEDFMATASGGLGFALPAVGAIAQPDRT 433
RESULT 15
Q7SG34 PRELIMINARY; PRT; 540 AA.
AC Q7SG34
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU07508.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Sella S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0-0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000013; EAA35819.1; -.
```

```
SQ SEQUENCE 540 AA; 60340 MW; BCAB82CBE127046F CRC64;
  Query Match 11.4%; Score 76; DB 2; Length 540;
  Best Local Similarity 23.6%; Pred. No. 57;
  Matches 34; Conservative 19; Mismatches 57; Indels 34; Gaps 5;
QY 5 PMQPTSTANKIIVSDPTRLSTTFSASLLRQKVKVGI-AELNNVSGQYVSVY----- 55
Db 27 PKQPL-----FSDVSHLLTHCSSKSHLSHRFKTEIRARHNDAAARETIQQYLKWEES 78
QY 56 -----KRPAP--KPEGCADACVIMPNENQSIPTVIGSAENLATLKAWE 98
Db 79 GIHALLEDLEAKENKKPKRGRPAGTANRPKAFQNRDDLVRNEAAGEQLDHTPVLAWHI 138
QY 99 THKRNVDTLFASGNAGLGFLDPTA 122
Db 139 TDPNNASQFQHNLRHGHGYLDPPA 162
Search completed: June 1, 2005, 09:45:53
Job time : 117 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:34:17 ; Search time 114 Seconds
(without alignments)
588.442 Million cell updates/sec

Title: US-10-617-876-3

Perfect score: 666

Sequence: 1 MANKTQPTSTANKIWSDD.....NAGLGFLDPTAAIVSSDDTTA 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	99.1	131	Q9AZ42	Q9az42 bacteriophage
2	84.5	12.7	667	Q6LQ87	Q6lq87 photobacter
3	80	12.0	194	1 LPK MYCLE	Q49803 mycobacteri
4	79	11.9	918	1 L6B HUMAN	P40189 homo sapien
5	78	11.7	305	2 Q9RT24	Q9rt24 deinococcus
6	78	11.7	524	2 Q42147	Q42147 xenopus lae
7	78	11.7	524	2 Q42147	Q42147 xenopus lae
8	78	11.7	6146	2 Q8AVN9	Q8avn9 xenopus lae
9	77.5	11.6	1174	2 Q93HJ5	Q93hj5 streptomyce
10	77.5	11.6	1174	2 Q8MPR0	Q8mpr0 crassostrea
11	77	11.6	1454	2 Q8ENZ2	Q8enz2 oceanobacil
12	77	11.6	373	2 Q74KV6	Q74kv6 lactobacill
13	76.5	11.5	457	2 Q6C3F9	Q6czum6 homo sapien
14	76.5	11.5	546	1 CH60 CHRVI	Q6c3f9 yarrowia li
15	76.5	11.5	988	2 Q87ID1	P31293 chromatiu
16	76	11.4	436	2 Q74BT9	Q87idi vibrio para
17	75.5	11.3	519	1 ACHG BOVIN	Q74bt9 geobacter s
18	75.5	11.3	538	2 Q7WSS8	P13536 bos taurus
19	75	11.3	386	2 Q8P9T4	Q7ws88 pseudomonas
20	75	11.3	711	2 Q6MKR4	Q8p9t4 xanthomonas
21	75	11.3	881	2 Q7RM96	Q6mkra bdellovibri
22	74	11.1	559	2 Q26645	Q7rm96 plasmodium
23	74	11.1	620	2 Q12623	Q26645 strongyloce
24	74	11.1	713	2 Q8EV63	Q12623 humicola gr
25	74	11.1	1084	2 Q6BGK7	Q8ev63 mycoplasma
26	74	11.1	1693	2 Q7RLG9	Q6bgk7 paramacium
27	74	11.1	1851	2 Q8JUF5	Q7rlg9 plasmodium
28	74	11.1	2799	1 G112 HUMAN	Q8juf5 bean pod mo
29	73.5	11.0	213	2 Q50402	Q8juf5 mycobacteri
30	73.5	11.0	291	2 Q9S8F9	Q50402 mycobacteri
31	73.5	11.0	296	2 Q7TWL6	Q9s8f9 arabidopsis
					Q7twl6 mycobacteri

32 73.5 11.0 453 2 Q8D688
33 73.5 11.0 830 2 Q9U3V0
34 73.5 11.0 831 2 Q92DZ6
35 73.5 11.0 1845 2 Q86JH8
36 73.5 11.0 7048 2 Q6D739
37 73 11.0 214 2 Q9SXH1
38 73 11.0 547 2 Q8V5Y8
39 73 11.0 1416 2 Q897I8
40 73 11.0 1850 2 Q9YUJ5
41 73 11.0 1851 2 Q8JUF2
42 72.5 10.9 286 2 Q72SY0
43 72 10.8 273 1 FWDC METJA
44 72 10.8 517 2 Q8FEB3
45 72 10.8 680 2 Q9N9G7

ALIGNMENTS

RESULT 1

Q9AZ42 PRELIMINARY; PRT; 131 AA.

AC Q9AZ42;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Coat protein.
OS Bacteriophage AP205.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=154784;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22024855; PubMed=12029168;
RA Klovins J., Overbeek G.P., van den Worm S.H., Ackermann H.W.,
RA van Duijn J.;
RT "Nucleotide sequence of a ssRNA phage from Acinetobacter: kinship to
RT coliphages.";
RL J. Gen. Virol. 83:1523-1533(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Klovins J.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334111; AAK20390.1; -
DR GO; GO:0019028; C:vital capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
KW Coat protein.
SQ SEQUENCE 131 AA; 14009 MW; FB4ECBCEB8E129B2 CRC64;

Query Match 99.1%; Score 660; DB 2; Length 131;

Best Local Similarity 99.2%; Pred. No. 7.5e-59;

Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKTQPTSTANKIWSDDPTLSTFASLIRQVKVIGIAELNNVSGOYVSYKRPAP 60

Db 1 MANKTQPTSTANKIWSDDPTLSTFASLIRQVKVIGIAELNNVSGOYVSYKRPAP 60

Qy 61 KPQGCADACVIMENQSIQRTVIGSSAENLATLKAWEETHKRNVDITLFASSNAGLGFLDP 120

Db 61 KPQGCADACVIMENQSIQRTVIGSSAENLATLKAWEETHKRNVDITLFASSNAGLGFLDP 120

Qy 121 TAAIVSSDDTTA 131

Db 121 TAAIVSSDDTTA 131

RESULT 2

Q6LQ87 PRELIMINARY; PRT; 667 AA.

AC Q6LQ87;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

```
DE Hypothetical methyl-accepting chemotaxis protein.
GN Names=PSPT0323; OrderedLocNames=PPRA2077;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378669; CAC20479.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004089; Chmtaxis transd.
DR InterPro; IPR003660; His_kin_HAMP.
DR InterPro; IPR000727; T_SNARE-.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; MA; 1.
DR PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
DR PROSITE; PS50885; HAMP; 1.
DR PROSITE; PS50192; T_SNARE; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 667 AA; 73612 MW; 81D05DE30D60532C CRC64;

Query Match 12.7% Score 84.5; DB 2; Length 667;
Best Local Similarity 25.5%; Pred. No. 10;
Matches 36; Conservative 22; Mismatches 52; Indels 31; Gaps 6;

QY 2 ANKTMQPIIT-----STANKIVMSDPRLSTFTSASLLRQVRKVGIAELNNVSGQYVSVY 55
DB 420 ANETMQVITAINEMASTAEVARTTNTVNTHTNATVAADQSK---AAVNKATDSVALLM 476
QY 56 KRPAKPEGCADACVIMPNENQSIPTVIS-----GSAENLATLKAETHKRVNVDTLFAS 110
DB 477 TQIETASENVTE---MSNETQKISTVLNVIRDIAEQTNLLALNAATEAAR-----A 524
QY 111 GNAGLGLDPTAAIVSSDTTA 131
DB 525 GDQGRGF-----AVVADEVRA 540

RESULT 3
LPPK_MYCLE
ID _LPPK_MYCLE STANDARD; PRT; 194 AA.
AC Q49803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative lipoprotein lppk precursor.
GN Name=lppk; OrderedLocNames=ML1315;
GN ORFNames=MLCB2533.l1c, B2126_F3_l15;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TW;
RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E.,

Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus."
RL Nature 409:1007-1011(2001).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: Belongs to the MTB12 family.
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CC
DR EMBL; U00017; AAA17217.1; -.
DR EMBL; AL035310; CAA22925.1; -.
DR EMBL; AL583921; CAC31696.1; -.
DR PIR; S72877; S72877.
DR Leproma; ML1315; -.
DR InterPro; IPR000437; Prok_lipoprot_S.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
KW Palmitate; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 194 Putative lipoprotein lppk.
FT LIPID 27 27 S-diacylglycerol cysteine (By
FT LIPID 27 27 similarity).
FT LIPID 27 27 N-palmitoyl cysteine (By similarity).
SQ SEQUENCE 194 AA; 20460 MW; E975262FC3218A86 CRC64;

Query Match 12.0% Score 80; DB 1; Length 194;
Best Local Similarity 25.0%; Pred. No. 6.5;
Matches 30; Conservative 10; Mismatches 26; Indels 54; Gaps 6;

QY 8 PITSTANKIVMS--DPTRLSTFTSASLLRQVRKVGIAELNNVSGQYVSVYK-----RPAP 60
DB 110 PMTFTANNIAWSKNKPSDVLATIS-----VNIAQTNN-----SVSPFPMETFPF 154
QY 61 KPESCADACVIMPNENQSIPTVISGSAENLATLKAETHKRVNVDTLFASGNAGLGLDLP 120
DB 155 PPQ-----QSWLSKRTADMLLEFGNSS-GLTNP 182

RESULT 4
IL6B_HUMAN
ID _IL6B_HUMAN STANDARD; PRT; 918 AA.
AC P40189; Q9U041;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (gp130) (Oncostatin M
DE receptor) (CDw130) (CD130 antigen).
GN Name=IL6ST;
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOPFORM 1).
RC TISSUE=Myeloma, and Placenta;
RX MEDLINE=91084844; PubMed=2261637; DOI=10.1016/0092-8674(90)90411-7;
RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
RT "Molecular cloning and expression of an IL-6 signal transducer,
RT gp130."
RL Cell 63:1149-1157(1990).
```

RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Synovium; PubMed=10880057;
 RX MEDLINE=20341529; PubMed=10880057;
 RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
 RA Murakami M., Nakao K.;
 RT "Cloning of novel soluble gp130 and detection of its neutralizing
 RT autoantibodies in rheumatoid arthritis.";
 RL J. Clin. Invest. 106:137-144 (2000).
 RN [3]
 RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=21269398; PubMed=11098061; DOI=10.1074/jbc.M009979200;
 RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
 RT "Determination of the disulfide structure and N-glycosylation sites of
 RT the extracellular domain of the human signal transducer gp130.";
 RL J. Biol. Chem. 276:8244-8253 (2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE=98169383; PubMed=9501088; DOI=10.1093/emboj/17.6.1665;
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674 (1998).
 CC -I- FUNCTION: Signal-transducing molecule. The receptor systems for
 CC IL6, LIF, OSM, CNTF, IL11 and CT1 can utilize gp130 for initiating
 CC signal transduction. Binds to IL6/IL6R (alpha chain) complex,
 CC resulting in the formation of high-affinity IL6 binding sites, and
 CC transduces the signal. Does not bind IL6. May have a role in
 CC embryonic development (By similarity).
 CC -I- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
 CC Secreted (isoform 2).
 CC -I- ALTERNATIVE PRODUCTS.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P40189-1; Sequence=Displayed;
 CC Name=2; Synonyms=GP130-RAPS;
 CC IsoId=P40189-2; Sequence=VSP_001684, VSP_001685;
 CC -I- TISSUE SPECIFICITY: Found in all the tissues and cell lines
 CC examined. Expression not restricted to IL-6 responsive cells.
 CC -I- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -I- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -I- DISEASE: Isoform 2 is an autoantigen found in rheumatoid arthritis
 CC (RA) but it is not specific to patients with RA.
 CC -I- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 2.
 CC -I- SIMILARITY: Contains 5 fibronectin type III domains.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -I- DATABASE: NAME=PROW; NOTE=CD guide CD130 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
 CC -----
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 CC -----
 CC EMBL; M57230; AAA59155.1; --
 CC EMBL; AB015706; BAA78112.1; --
 CC PIR; A36337; A36337.
 CC PDB; 1BJ8; NMR; @=217-325.
 CC PDB; 1BQJ; X-ray; A/B=119-333.
 CC PDB; 1IIR; X-ray; A=23-325.
 CC Genew; HGNC:6021; IL6ST.
 CC MIM; 600694; --
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004915; F:interleukin-6 receptor activity; TAS.
 CC GO; GO:0004924; F:oncostatin-M receptor activity; TAS.
 CC GO; GO:0004872; F:receptor activity; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003529; Hemptrecept_1302.
 DR InterPro; IPR010457; Lep_receptor_Ig.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF06328; Lep_receptor_Ig; 1.
 DR PROSITE; PS0853; FN3; 5.
 DR PROSITE; PS01353; HEMATOPO REC L F2; 1.
 KW 3D-structure; Alternative splicing; Direct protein sequencing;
 KW Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Interleukin-6 receptor beta chain.
 FT CHAIN 23 918 Extracellular (Potential).
 FT DOMAIN 23 619 Potential.
 FT TRANSMEM 620 641 Cytoplasmic (Potential).
 FT DOMAIN 642 918 Ig-like C2-type.
 FT DOMAIN 26 120 Fibronectin type-III 1.
 FT DOMAIN 125 216 Fibronectin type-III 2.
 FT DOMAIN 222 321 Fibronectin type-III 3.
 FT DOMAIN 326 418 Fibronectin type-III 4.
 FT DOMAIN 423 514 Fibronectin type-III 5.
 FT DOMAIN 518 610 Ser-rich.
 FT DOMAIN 725 755 WSXWS motif.
 FT SITE 310 314 Box 1 motif.
 FT SITE 651 659
 FT DISULFID 28 54
 FT DISULFID 48 103
 FT DISULFID 134 144
 FT DISULFID 172 182
 FT DISULFID 458 466
 FT CARBOHYD 43 43 N-linked (GlcNAc...)
 FT CARBOHYD 83 83 N-linked (GlcNAc...)
 FT CARBOHYD 131 131 N-linked (GlcNAc...)
 FT CARBOHYD 157 157 N-linked (GlcNAc...)
 FT CARBOHYD 227 227 N-linked (GlcNAc...)
 FT CARBOHYD 379 379 N-linked (GlcNAc...)
 FT CARBOHYD 383 383 N-linked (GlcNAc...)
 FT CARBOHYD 553 553 N-linked (GlcNAc...)
 FT CARBOHYD 564 564 N-linked (GlcNAc...)
 FT VARSPLIC 325 329 RPSKA -> NIASF (in isoform 2).
 FT VARSPLIC 330 918 Missing (in isoform 2).
 FT STRAND 29 32 /FTId=VSP_001685.
 FT STRAND 37 39
 FT TURN 40 41
 FT STRAND 44 50
 FT HELIX 52 58
 FT TURN 59 59
 FT TURN 62 64
 FT STRAND 65 69
 FT TURN 70 71
 FT STRAND 72 73
 FT STRAND 76 78
 FT HELIX 80 83
 FT STRAND 84 85
 FT TURN 86 91
 FT STRAND 98 107
 FT TURN 108 110
 FT STRAND 111 123
 FT STRAND 130 137
 FT TURN 138 139
 FT STRAND 143 147
 FT STRAND 157 164
 FT TURN 165 166
 FT STRAND 167 168
 FT TURN 172 173
 FT TURN 179 180
 FT STRAND 181 183
 FT TURN 190 191

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FT STRAND 194 202
FT TURN 203 204
FT STRAND 205 208
FT STRAND 212 214
FT HELIX 216 219
FT STRAND 220 221
FT STRAND 226 231
FT STRAND 240 245
FT STRAND 248 251
FT TURN 252 252
FT STRAND 255 263
FT TURN 264 265
FT STRAND 270 271
FT HELIX 274 277
FT STRAND 283 286
FT TURN 291 292
FT STRAND 294 303
FT TURN 304 305
FT STRAND 317 320
SQ SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;

Query Match 11.9%; Score 79; DB 1; Length 918;
Best Local Similarity 25.5%; Pred. No. 55;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVMSDPTRLSTTPSASILLR-ORVKVGIAELNNVSGQVSVYKRPAPKPGCAD 67
Db 82 INFTASSVTFDTASLNQICNLTFGQLEQNVYGTIISG-----LPPEKPKNL-- 132

QY 68 ACVIMPNENOSIRTVISGSAENLA----TLKAEWETHK 101
Db 133 SCIV--NEGKMKRCWDGGRETHLETNFTLKSEWATHK 168

RESULT 5
Q9RT24 PRELIMINARY; PRT; 305 AA.
AC Q9RT24;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DE Malonyl CoA-acyl carrier protein (transacylase)
GN OrderedLocusNames=DR1945;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Uitterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL; AE002033; AAF11497.1; -.
DR PIR; A75334; A75334.
DR HSP; P25715; IMLA.
DR TIGR; DR1945; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004314; F:acyl-carrier protein[S-malonyl]transferase. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001227; Ac:transferase.
DR InterPro; IPR004410; FabD.
DR Pfam; PF00698; Acyl_transf_1; 1.
DR TIGRFAMS; TIGR00128; fabD; 1.

KW Complete proteome.
SQ SEQUENCE 305 AA; 31284 MW; 0564188B9FA35E9F CRC64;

Query Match 11.7%; Score 78; DB 2; Length 305;
Best Local Similarity 28.9%; Pred. No. 18;
Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;

QY 13 ANKIVMSDPTRLSTTPSASILLRQVRVKVGIAELNNVSGQVSVYKRPAPKPGC-ADACVI 71
Db 103 AGVITLEDALRL-TRKRGELMQQAVPEGVGMSAVMGD-----PAVVAEVCQAQGVV 154

QY 72 MP-NENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGLDPTAAIVSSDIT 130
Db 155 QPANFNAPTQTVISGEKAAVDAASAEKTRGLKAIPKVSAPPHCALMRPAEGLSAELH 214

QY 131 A 131
Db 215 A 215

RESULT 6
O42147 PRELIMINARY; PRT; 524 AA.
ID O42147;
AC O42147;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE DarBP-Zfa.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97415754; PubMed=9268652; DOI=10.1006/jmbi.1997.1177;
RA Finerty P.J., Jr., Bass B.L.;
RT "A Xenopus zinc finger protein that specifically binds dsRNA and RNA-
RL DNA hybrids."
RL J. Mol. Biol. 271:195-208(1997).
DR EMBL; AF005083; AAC60260.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR003604; Znf_U1.
DR SMART; SM00355; Znf_C2H2; 7.
DR SMART; SM00451; Znf_U1; 7.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
DR PROSITE; PS00028; ZINC FINGER_C2H2_1; UNKNOWN 7.
SQ SEQUENCE 524 AA; 55588 MW; 104D66038ADB8D57 CRC64;

Query Match 11.7%; Score 78; DB 2; Length 524;
Best Local Similarity 26.9%; Pred. No. 35;
Matches 42; Conservative 20; Mismatches 62; Indels 32; Gaps 8;

QY 2 ANKTMPIITSTA--NKIVMSDPTRL-----STFASILL-----RQVRKVGIAEL 44
Db 139 AKKTRTPTVATKSDNKMDSHSDRAKFCCLKHSTFNNPLMAEQHVAGKKHKKQETKTQIMTI 198

QY 45 NNVSQGVSVYKRP-----APKP-EGCA-----DACVIMPNENOSIRTVISGSAEN---L 90
Db 199 YTSGGQTTPAQAPIPLNLSNFMFGSGAGKGFCDKCNIVLNSIEQYQAHVSGAKHKQLM 258

QY 91 ATLKAETHKRNVDTLFASGNAGLGLDPTAAIV 125
Db 259 SMTPLSEEGHQAQVAPSAIASGAGKGFCDTCNIV 294

RESULT 7
Q8AVN9 PRELIMINARY; PRT; 524 AA.
ID Q8AVN9
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Best Local Similarity 36.1%; Pred. No. 7.2e+02;
Matches 35; Conservative 10; Mismatches 42; Indels 10; Gaps 4;

QY 24 LSTTFASLRLQKVKVIGIAELNNVSGQVSVYKRPAPKPEGCA----DACVIMPENQSI 79
DB 3100 LSLDGAALVTLASRL-IAELSCHGGVSVASPADTAERIARWNGGICVAANSERS- 3157

QY 80 RTVWISGAENLATLKAWE---THKRNVDTLFASGNA 113
DB 3158 -TVVSGPEALAECEAEGVRARRIPVDYASHSA 3193

RESULT 9
Q8MERO Q8MERO PRELIMINARY; PRT; 1174 AA.
AC Q8MERO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Bone morphogenetic protein type 2 receptor.
GN Name=BMP-R2 Gene;
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RA Herpin A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ427420; CAD20574.1; -.
DR HSSP; P36897; I1AS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004572; F:protein kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007178; P:transmembrane receptor protein serine/threo. .; IEA.
DR InterPro; IPR000472; Activin receptor.
DR InterPro; IPR000333; Actn_receptorII.
DR InterPro; IPR011003; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR PRINTS; PR00653; ACTIVIN2R.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Receptor.
SQ SEQUENCE 1174 AA; 132154 MW; 5E3928BD1406507A CRC64;

Query Match 11.6%; Score 77.5; DB 2; Length 1174;
Best Local Similarity 26.9%; Pred. No. 1.1e+02;
Matches 36; Conservative 23; Mismatches 48; Indels 27; Gaps 8;

QY 5 TMQPIITSTANKI-VWSDPTLSTTFASLRLQKVKVIGIAE-----LNNVSGQVYV---- 52
DB 686 TPTTITTSFQISSESPERTHPTTA-MAPTEETGTADNSTASVMVINSPPNGYITSRP 744

QY 53 -SVYKRPAPKPEG-CADACVIM-PENQSI---IRTVISGAENLATLK-----AEWE 98
DB 745 SSWYNRGMTTSGTSTTFVWMSPEDEAPPVKLVNNAKNNVLPVHQGRIPIAERN 804

QY 99 THKRNVDTLFASGNA 112
DB 805 THKRSDELSVSGN 818

RESULT 10
Q8ENZ2 Q8ENZ2 PRELIMINARY; PRT; 1454 AA.
AC Q8ENZ2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Bacillopeptidase F (EC 3.4.21.-).
GN OrderedLocusNames=OB2331;

OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments."
RT Nucleic Acids Res. 30:3927-3935 (2002).
CC -I- SIMILARITY: Belongs to peptidase family S8.
DR EMBL; AF004600; BAC14287.1; -.
DR HSSP; Q99405; LMPT.
DR MEROPS; S08.017; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR009020; Prot_inh_S8A.
DR InterPro; IPR010259; Prot_inh_S8A.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF05922; Subtilisin_N; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Complete proteome; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 1454 AA; 155494 MW; 9223ADF205D7FF7F CRC64;

Query Match 11.6%; Score 77.5; DB 2; Length 1454;
Best Local Similarity 29.4%; Pred. No. 1.4e+02;
Matches 25; Conservative 15; Mismatches 42; Indels 3; Gaps 1;

QY 47 VSCQYVSVYKRPAPKPEGCADACVIMPENQSI---IRTVISGAENLATLKAEWETHKRNVD 106
DB 165 VNGIATVTKKVAATTAETAEVEKILNETRELYTTVDKDAE---TPKSDVANVWNR 221

QY 107 LFASGNAGLGLDPTAAIVSSDTTA 131
DB 222 VGAPATWNGFGDSGVVASIDTGA 246

RESULT 11
Q74KV6 Q74KV6 PRELIMINARY; PRT; 373 AA.
AC Q74KV6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DNA polymerase IV.
GN OrderedLocusNames=LJ0471;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pidmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533."
RT Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).
DR EMBL; AE017201; AAS08463.1; -.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR001126; UMUC_like.
DR Pfam; PF00817; IMS; 1.
DR PROSITE; PS50173; UMUC; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 42240 MW; 3D2A1421FD195BE7 CRC64;
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Query Match 11.6%; Score 77; DB 2; Length 373;
Best Local Similarity 27.6%; Pred. No. 29;
Matches 21; Conservative 14; Mismatches 25; Indels 16; Gaps 3;

QY 12 TANKVMSDPTSLSTPESALLRQV--KVGIAE-----LNNVSGYVSVYKRPAP 60
DB 124 TENKLNLTDPRI-----ALLQRIYQRIGLTSSFGVSYNKLAKMGSEYAKPFGRTVI 178
QY 61 KPGECADACVMPNEN 76
DB 179 KPEGARDFLAKQPIKN 194

RESULT 12
Q6ZUM6 Q6ZUM6 PRELIMINARY; PRT; 1088 AA.
AC Q6ZUM6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ43536.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Placenta;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fuji A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AKI2524; BAC86194.1; -
FT NON TER 1088 1088
SQ SEQUENCE 1088 AA; 126002 MW; A08B75393ADC564A CRC64;

Query Match 11.6%; Score 77; DB 2; Length 1088;
Best Local Similarity 29.7%; Pred. No. 1.1e+02;
Matches 19; Conservative 15; Mismatches 14; Indels 16; Gaps 3;

QY 41 IAEIANNVSGYVSVYKRPAPKPGCADACVIMP-----NENQISRTVSGSAENLATLK 94
DB 963 VEIIGDANLQYKLOER--KPE-----ILPLFQEAEDKRLRLRTVAGGLETISNLK 1012
QY 95 AEWE 98
DB 1013 AKWD 1016

RESULT 13
Q6C3F9 Q6C3F9 PRELIMINARY; PRT; 457 AA.
AC Q6C3F9;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE Similar to sp|P08540 Kluyveromyces fragilis potential acid
DE phosphatase.
GN ORFName=YALI0E3222g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
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RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi R.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nikolski M., Oxtas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Pocher S., Richard G.F., Straub M.L., Suleau A.,
RA Swemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope; (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382131; CAG80411.1; -
DR GO; GO:0016788; F-hydrolase activity, acting on ester bonds; IEA.
DR InterPro; IPR007312; Pesterase.
DR Pfam; PF04185; Phosphoesterase; 1.
SQ SEQUENCE 457 AA; 50001 MW; 523BE4A48PB34C4C CRC64;

Query Match 11.5%; Score 76.5; DB 2; Length 457;
Best Local Similarity 23.7%; Pred. No. 42;
Matches 32; Conservative 20; Mismatches 34; Indels 49; Gaps 6;

QY 46 NVSGQVSVYKRP-APKPGCADACVIMP-NENQ-----SIRTVSGSA----- 87
DB 242 SVSGRYVTWVKKPLNLTNTTEFAKDSLIITFDENETYKQNSVLAILLGAVPHLRGTTD 301
QY 88 -----ENLATLKAWE-----THKRNVDI--LFASGNAGLG 116
DB 302 DTFYDHYSNLATVEANWELPHLGRGDVNAVFKFVADENIKRNISTEGLYNNASQPGY 361
QY 117 FLDPTAAIVSSDTTA 131
DB 362 FMDDTVPPIVVDLTA 376

RESULT 14
CH60 CH60 CH60 STANDARD; PRT; 546 AA.
AC P31253;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN Name=grol; Synonyms=groEL, mopA;
OS Chromatium vinosum.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC Chromatiaceae; Allochromatium.
OX NCBI_TaxID=1049;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93186721; PubMed=8444812;
RA Ferreyra R., Soncini F., Viale A.M.;
RT "Cloning, characterization, and functional expression in Escherichia
RT coli of chaperonin (groEL) genes from the phototrophic sulfur
RT bacterium Chromatium vinosum.";
RL J. Bacteriol. 175:1514-1523(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=99008942; PubMed=9790891; DOI=10.1006/prep.1998.0953;
RA Dionisi H.M., Viale A.M.;
RT "Purification and characterization of Chromatium vinosum GroEL and
RT GroES proteins overexpressed in Escherichia coli cells lacking the
RT endogenous groEL operon.";
RL Protein Expr. Purif. 14:275-282(1998).
CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
CC proper assembly of unfolded polypeptides generated under stress
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CC conditions.
CC -1- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
CC 7 subunits.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M99443; AAA23319.1; -.
CC PIR: B47073; B47073.
CC HSP: P06139; IGR5.
CC HAMAP: MF 00600; -.
CC InterPro: IPR001844; Chaperonin Cpn60.
CC InterPro: IPR002423; Cpn60/TCP-1.
CC InterPro: IPR008950; GroEL-ATPase.
CC Pfam: PF00118; Cpn60_TCP1; 1.
CC PRINTS: PR00298; CHAPERONIN60.
CC PRINTS: PR00304; TCOMPLEXTCP1.
CC PROSITE: PS00296; CHAPERONIN_CPN60; 1.
CC ATP-binding; Chaperone.
CC SQ SEQUENCE 546 AA; 57541 MW; 3250141881C04DD6 CRC64;

Query Match 11.5%; Score 76.5; DB 1; Length 546;
Best Local Similarity 20.7%; Pred. No. 52;
Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps 3;

QY 3 NKTQPIITSTANKI--VMSDPTLSTTFSASLLRQVRKVGIAELN-----NVS 48
Db 68 NMGAQMVKEVASKTSDTAGDGTATVLAQVMREGLKAVAGNPNMPLKRGMDKAVEAA 127

QY 49 GQYVSVYKRPAPKEGCADACVIMPENQSIQRTVVISGSAENL---ATLKAWEETHKRNVD 105
Db 128 TEELKLSKCPRPMAAQVGTISANSDDSGIIGIIAEMKEVKGVIITVEDGTSIQNEL 187

QY 106 TLFASGNAGLGFDDP 120
Db 188 DVVEGMOFDRGYLSP 202

RESULT 15
Q87ID1 Q87ID1 PRELIMINARY; PRT; 988 AA.
AC Q87ID1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sensor protein TorS.
GN OrderedLocuNames=VPA0675;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AP005086; BAC62018.1; -.
DR HSP: Q9A514; IMAV.
DR GO: GO:0016021; C:integral to membrane; IEA.
```

```
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0000156; F:two-component response regulator activity; IEA.
DR GO: GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO: GO:0007600; P:sensory perception; IEA.
DR GO: GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro: IPR003594; ATPbind ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR011006; CheY_like.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR003661; His_kin N.
DR InterPro: IPR003660; His_kin HAM.
DR InterPro: IPR009082; His_kin_homodim.
DR InterPro: IPR008207; Hpt.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF00672; HAM; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00512; Hsika; 1.
DR Pfam: PF01627; Hpt; 1.
DR Pfam: PF00072; Response_reg; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00304; HAM; 1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; Hsika; 1.
DR SMART: SM00073; HPT; 1.
DR SMART: SM00448; REC; 1.
DR PROSITE: PS0885; HAM; 1.
DR PROSITE: PS0109; HIS_KIN; 1.
DR PROSITE: PS0894; HPT; 1.
DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
KW transferase; Transmembrane.
SQ SEQUENCE 988 AA; 109882 MW; 962F67DF6A44BC72 CRC64;

Query Match 11.5%; Score 76.5; DB 2; Length 988;
Best Local Similarity 24.7%; Pred. No. 1.le+02;
Matches 36; Conservative 18; Mismatches 47; Indels 45; Gaps 6;

QY 1 MANKTQW---PITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVS----- 48
Db 295 LMQKTLFLFSELNSTVKNLV--DDSNKTTTFAVDQLTNTLKFAQWSLTIVISGLIIVVL 352

QY 49 ----GQYVSVYKRPAP-----KPE--GCADACVIMPENQSIQT 81
Db 353 ILWRVYVYVVKRLAELYSALLSVAQGNLALEVEVKGDELAHMGQAIIITARTAQAKV 412

QY 82 VISGSAENLATLKAWEETHKRNVDTL 107
Db 413 VAEGEAK----AKRELEEHKEHLEEL 434

Search completed: June 1, 2005, 09:45:54
Job time : 115 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:34:57 ; Search time 24 Seconds
(without alignments)
525.183 Million cell updates/sec

Title: US-10-617-876-3
Perfect score: 666
Sequence: 1 MANKTMQPTSTANKIWS.....NAGLGFLDPTAAIVSSDTTA 131
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	12.0	194	2 S72877	hypothetical prote
2	79	11.9	918	2 A36337	membrane glycoprot
3	78	11.7	305	2 A75334	acyl-carrier-prot
4	76.5	11.5	546	2 B47073	chaperonin GroEL -
5	75.5	11.3	519	2 I45847	acetylcholine rece
6	73.5	11.0	213	2 D70972	probable enoyl-coA
7	73.5	11.0	291	2 T51668	myb-related transc
8	73.5	11.0	831	2 A11515	ORF of Listeria s
9	73	11.0	547	2 AC1314	malolactic enzyme
10	72	10.8	273	2 B64446	formylmethanofuran
11	71.5	10.7	220	2 T14951	hypothetical prote
12	71.5	10.7	942	1 JQ1674	protein kinase TMK
13	71	10.7	562	2 S38149	SIS2 protein - yea
14	70.5	10.6	414	2 A86229	hypothetical prote
15	70.5	10.6	536	2 JG0022	flagellar basal-bo
16	70	10.5	519	2 I56566	nicotinic acetylch
17	70	10.5	519	2 S13874	hypothetical prote
18	69.5	10.4	358	2 T27862	hypothetical prote
19	69.5	10.4	358	2 S11407	(2'-5')oligo(A) sy
20	69.5	10.4	643	2 I50539	intermediate filam
21	69.5	10.4	26926	1 I38344	titin, cardiac mus
22	69	10.4	374	2 T10415	virus envelope pro
23	69	10.4	666	2 S29349	hypothetical prote
24	69	10.4	2187	2 S60224	polyketide synthas
25	68	10.2	252	2 C69172	conserved hypothet
26	68	10.2	267	2 A97762	hypothetical prote
27	68	10.2	350	2 S51494	arabinogalactan en
28	68	10.2	454	2 S16522	mitosis-specific c
29	67.5	10.1	330	2 T37854	probable IUNH-fam

30	67.5	10.1	577	2 H69354	probable fatty-aci
31	67.5	10.1	903	2 T09143	alpha-glucosidase
32	67.5	10.1	913	2 AC2445	hypothetical prote
33	67	10.1	143	2 T14664	hypothetical prote
34	67	10.1	398	2 E82262	hypothetical prote
35	67	10.1	507	2 B84506	probable Athila re
36	67	10.1	508	2 T16980	probable cytochrom
37	67	10.1	646	2 T17631	hypothetical prote
38	67	10.1	772	1 A44052	outer layer protei
39	67	10.1	1056	2 T33167	hypothetical prote
40	67	10.1	1286	2 S28634	adhesin AIDA-I pre
41	67	10.1	6805	2 S20901	titin - rabbit (fr
42	66.5	10.0	194	2 C86676	hypothetical prote
43	66.5	10.0	380	2 B70544	probable histidino
44	66.5	10.0	569	2 D96954	methyl-accepting c
45	66.5	10.0	625	2 C25977	phosphotransferase

ALIGNMENTS

RESULT 1

S72877
hypothetical protein B2126_F3_115 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72877
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B2126.
A;Reference number: S72585
A;Accession: S72877
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <SMI>
A;Cross-references: UNIPROT:Q49803; EMBL:U00017; NID:g466994; PIDN:AAAL7217.1; PID:g467070;
C;Genetics:
A;Start codon: GTG

Query Match 12.0%; Score 80; DB 2; Length 194;
Best Local Similarity 25.0%; Pred. No. 1.1;
Matches 30; Conservative 10; Mismatches 26; Indels 54; Gaps 6;

QY	8	PITSTANKIWS--DPTRLSTTFSASLLRQVKVKGIAELNNVSGQYVYK-----RPAP 60
Db	110	PMFTANNIAWSKNPDSVLATIS-----VNIAQTNN-----SVFSPFMEFTFPF 154
QY	61	KPEGCADACVIMPENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db	155	PFQ-----QSQWLKSKRTADMILLEFGNSS-GLTNP 182

RESULT 2

A36337
membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
C;Accession: A36337
R;Hibi, M.; Murakami, M.; Saico, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Accession: A36337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-918 <HIB>
A;Cross-references: UNIPROT:P40189; GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
C;Genetics:
A;Gene: GDB:IL6ST; GP130
A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>

Query Match 11.9%; Score 79; DB 2; Length 918;
Best Local Similarity 25.5%; Pred. No. 9.3;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVMSDPRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPGCCAD 67
Db 82 INRTASSVTFDTIASLNLIQTNCNLTTFQGLEQNVYGITIISG-----LPPEKPKNL-- 132
Qy 68 ACVIMPNENOSIRTVISGSAENLA---TLKAEWETHK 101
Db 133 SCIV--NEGKMKRCWGDGGRHLETHLFTNFTLKSEWATHK 168

RESULT 3
A75334
[acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) DRI945 [similarity] - Deinococcus
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: A75334
R:White, O.; Eissen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-305 <WHI>
A:Cross-references: UNIPROT:Q9RT24; GB:AE002033; GB:AE000513; NID:g6459726; PIDN:AAF1149
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRI945
A:Map position: 1
C:Superfamily: [acyl-carrier-protein] S-malonyltransferase; [acyl-carrier-protein] S-mal
C:Keywords: acyltransferase; coenzyme A
F:7-286/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F:93/Active site: Ser (covalent substrate-binding) #status predicted
F:198/Active site: His #status predicted

Query Match 11.7%; Score 78; DB 2; Length 305;
Best Local Similarity 28.9%; Pred. No. 3.1;
Matches 35; Conservative 14; Mismatches 62; Indels 10; Gaps 4;

Qy 13 ANKIVMSDPRLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAPKPGC-ADACVI 71
Db 103 AGVLTLEDAURL-TRKGELMQQAVPGVGAMSVMGD-----PAVVAEVCQAQGVV 154
Qy 72 MP-NENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGLDPTAAIVSSDIT 130
Db 155 QPANFNAPTQTVISGEKAAVDAASAEUKTRGLKAIPLKVSAPFHCALMRPAEGLSALH 214
Qy 131 A 131
Db 215 A 215

RESULT 4
B47073
Chaperonin GroEL - Chromatium vinosum
C:Species: Chromatium vinosum
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B47073
F: Ferreyra, R.G.; Soncini, F.C.; Viale, A.M.
J. Bacteriol. 175, 1514-1523, 1993
A:Title: Cloning, characterization, and functional expression in Escherichia coli of cha
A:Reference number: A47073; MUID:93186721; PMID:8444812
A:Accession: B47073
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-546 <FR>
A:Cross-references: UNIPROT:P31293; GB:M99443; NID:g145007; PIDN:AAA23319.1; PID:g145009

A;Note: sequence extracted from NCBI backbone (NCBIN:126968, NCHIP:126970)
C;Superfamily: chaperonin groEL
C;Keywords: molecular chaperone

Query Match 11.5%; Score 76.5; DB 2; Length 546;
Best Local Similarity 20.7%; Pred. No. 9;
Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps

QY 3 NKTWQPIITANKI--VMSDPTRLSTTFSSASLLRQVRKVGIAEIN-----NVSV
DB 68 NMGAQMVKEVASKTSDIAGDGTITATVLAQAMVREGLKAVAGMNPMDLKRGMDKAVAAEA
QY 49 GQYVSVYKRPAPKEGCACAVIMPENQSIQRTVIGSAAENL---ATLKAETHETHKRNVD
DB 128 TEELUKLSKCPPRMAIAQVGTITANSDDSIGITIIAEMKEVKEGVITVEDGTSLQNEH
QY 106 TLFASGNAGLGFLDP 120
DB 188 DVEGMOQFDRGYLSP 202

RESULT 5
145847
acetylcholine receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2000
C;Accession: I45847
R;Takai, T.; Noda, M.; Furutani, Y.; Takahashi, H.; Notake, M.; Shimizu, S.
Eur. J. Biochem. 143, 109-115, 1984
A;Title: Primary structure of gamma subunit precursor of calf-muscle acetylcholine receptor
A;Reference number: I45847; MUID:84285374; PMID:6547904
A;Accession: I45847
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: mRNA
A;Residues: 1-519 <TAK>
A;Cross-references: UNIPROT:P13536; GB:M28307; NID:g162601; PIDN:AAA30351
C;Genetics:
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match 11.3%; Score 75.5; DB 2; Length 519;
Best Local Similarity 23.4%; Pred. No. 11;
Matches 37; Conservative 20; Mismatches 62; Indels 39; Gaps

QY 2 ANKTMQPIITANKIVMSDPTRLSTTFSSASLLRQVRKVGIA-----ELNNVSGQ---
DB 370 AHPRLQNGSSGWPITAGEVALCLPRSELLFRQQRGLVRAALEKLEKGPESGQSP
QY 52 VSVYKRPAPKEGCACAVIMPENQSIQRTVIGSAAENLATLKAETHETHKRNVD-----
DB 430 CGSLQQAAPAIQACVEACNLIAARHQOHTFDSGN-----KEWFLVGRVLDRCVFL
QY 106 --TLFASGNAGLGFL-----DPTAIVSSD 128
DB 482 MSLSLFVCGTAGIFLMAHYNRVPALPPFGDPRSLPSSD 519

RESULT 6
D70972
probable enoyl-coA hydratase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2001
C;Accession: D70972
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, E.;
Konrad, M.A.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, M.;
Rejmanek, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, A.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70972
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-213 <COL>
A;Cross-references: UNIPROT:O50402; GB:AL009198; GB:AL123456; NID:g3242262; PIDN:CAA1575
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: echA18
C;Superfamily: Naphthoate synthase

Query Match 11.0%; Score 73.5; DB 2; Length 213;
Best Local Similarity 27.6%; Pred. No. 5.8;
Matches 24; Conservative 14; Mismatches 42; Indels 7; Gaps 3;

QY 33 LRORVKVGTAEIENVSGQYVSV---YKRPAPKPGACACVIMPNENOSIRTVISGSAE 88
Db 1 MRRRWTKMDKDEASPCGGDIEAWCQIMREQPPAEGVDRVALQRHNVALLITLSPQQA 60
QY 89 NLATLKAWEETHKRNVDITLFAAGNAGL 115
Db 61 NALNL-ASWRRLKRLDLL--AGESGL 84

RESULT 7
T51668
myb-related transcription factor MYB61 [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51668
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J.
Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-275, 1998
A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from A.
A;Reference number: Z14349; MUID:9839469; PMID:9839469
C;Accession: T51668
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-291 <KRA>
A;Cross-references: UNIPROT:Q9SBP9; EMBL:AF062896; PIDN:AAC83618.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: MYB61
A;Map position: I
C;Keywords: transcription factor

Query Match 11.0%; Score 73.5; DB 2; Length 291;
Best Local Similarity 21.9%; Pred. No. 8.5;
Matches 30; Conservative 21; Mismatches 67; Indels 19; Gaps 4;

QY 3 NKTMQPITSTANKIVWSDPTRLSTTFSASLLRQVRKVGTAEIENVSV-----QQY 51
Db 78 HKSPSSSSATNQDFLERPSDLSDFGQKLNFSNLGLSVTTDSSLCSMIPPQSPGNN 137

QY 52 V-SVYKRPAPKPGACACVIMPNENOSIRTVISGSAENLATLKAWEETHKRNVDITLFA 110
Db 138 VGSVLQTPV-----CVKPSLSLPHDNNSSPSISGDHVKLAPNWEFQTNNTSNFF-- 190

QY 111 GNAGLGFLDPTAAIVSS 127
Db 191 DNGGFSWSIPNSTSS 207

RESULT 8
A11515
ORF of *Listeria seeligeri*, (LPXTG motif) homolog lin0665 [imported] - *Listeria innocua*
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11515
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <GLA>
A;Cross-references: UNIPROT:Q9V5Y8; GB:NC_003210; PIDN:CAC99993.1; PID:g16411368; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1915
C;Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 11.0%; Score 73; DB 2; Length 547;
Best Local Similarity 25.0%; Pred. No. 20;
Matches 33; Conservative 21; Mismatches 56; Indels 22; Gaps 4;

QY 12 TANKIVWSDPTRLSTTFSASLLRQVRKVGTAEIENVSGQVSVYKRPAPK-----PEGC 65
Db 191 TNNETLLNDPLYLG-----NKRPLSESEDAFIASFVNVKVEFPFKAILHWEDPGR 242

QY 66 ADACVIMPNENOSIRTV-----ISGS-----AENLATLKAWEETHKRNVDITLFAAGNAGLGF 117
Db 243 ANASRILHNYRDKICTFNDIIOQTGAVVAVALTIQVSRIPLSQKIIIFGAGTAGIGI 302

QY 118 LDPTAAIVSSDT 129
Db 303 ADLSAQLMRET 314

RESULT 10
B64446
formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - *Methanococcus jannaschii*
C;Species: *Methanococcus jannaschii*
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11515
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-831 <GLA>
A;Cross-references: UNIPROT:Q92D26; GB:AL592022; PIDN:CAC95897.1; PID:g16413105; GSPDB:C
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin0665

Query Match 11.0%; Score 73.5; DB 2; Length 831;
Best Local Similarity 25.8%; Pred. No. 30;
Matches 34; Conservative 18; Mismatches 53; Indels 27; Gaps 7;

QY 8 PITSTAN-KIVWSDPTRLSTTFSASLLRQVRKVGTAEIENVSGQ-----YVSVYKRPAP-- 60
Db 646 PLVSDMNDKVKGVPGDYEVTLNA-----VNEDGAAEAKTFFIVRLKSPAPII 694

QY 61 --KPEGCACACVIMPNENOSIRTVISGSAENLATL-----KAWEETHKRNVDITLFAAGNA 113
Db 695 TVDPEVSYDSAIL-KNETELLKEVRAKTNDNSAITSADAPDKVKWQTPGSGYTVTLNAVND 753

QY 114 GLGFLDPTAAIV 125
Db 754 GIP-ADPVTFFIV 764

RESULT 9
AC1314
malolactate enzyme (malate dehydrogenase) homolog lmo1915 [imported] - *Listeria monocytogenes*
C;Species: *Listeria monocytogenes*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1314
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <GLA>
A;Cross-references: UNIPROT:Q9V5Y8; GB:NC_003210; PIDN:CAC99993.1; PID:g16411368; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1915
C;Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 11.0%; Score 73; DB 2; Length 547;
Best Local Similarity 25.0%; Pred. No. 20;
Matches 33; Conservative 21; Mismatches 56; Indels 22; Gaps 4;

QY 12 TANKIVWSDPTRLSTTFSASLLRQVRKVGTAEIENVSGQVSVYKRPAPK-----PEGC 65
Db 191 TNNETLLNDPLYLG-----NKRPLSESEDAFIASFVNVKVEFPFKAILHWEDPGR 242

QY 66 ADACVIMPNENOSIRTV-----ISGS-----AENLATLKAWEETHKRNVDITLFAAGNAGLGF 117
Db 243 ANASRILHNYRDKICTFNDIIOQTGAVVAVALTIQVSRIPLSQKIIIFGAGTAGIGI 302

QY 118 LDPTAAIVSSDT 129
Db 303 ADLSAQLMRET 314

RESULT 10
B64446
formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - *Methanococcus jannaschii*
C;Species: *Methanococcus jannaschii*
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

C;Accession: B64446
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woeser, C.
A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*.
A;Reference number: A64300; MUID:96337999; PMID:868087
A;Accession: B64446
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-273 <BUL>
A;Cross-references: UNIPROT:Q59571; GB:U67558; GB:I77117; NID:gl591786; PIDN:AAB99173-1.1
C;Genetics:
A;Map position: FOR1110572-1111393
C;Superfamily: Formylmethanofuran dehydrogenase, subunit C
C;Keywords: iron-sulfur protein; metalloprotein; oxidoreductase; tungsten

Query Match 10.8%; Score 72; DB 2; Length 273;
Best Local Similarity 27.6%; Pred.No.11;
Matches 27; Conservative 14; Mismatches 31; Indels 26; Gaps 4;

QY 34 RQRKVGVG--IAELNVVSGQVSVYKRPAPK-----PEGCADACVIMPNE 76
Db 43 RKRIKADIVDFVELNDGSEPRIVKNSPKLYIGSKMTKGIVVEG--DAGMYGAEM 100
QY 77 QSTRTVIGSAGNATLKAETHKRNVDTLFASGNAG 114
Db 101 KGGKIVVNGAES-----WAGQNMKGGLIKGNAG 131

RESULT 11
T14951
Hypothetical protein Y1035 - *Yersinia pestis* plasmid pMT1.
C;Species: *Yersinia pestis*
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14951
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.P.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the *Yersinia pestis* KIMS plasmid
A;Reference number: Z18268; MUID:99043898; PMID:98266348
A;Accession: T14951
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-220 <LIN>
A;Cross-references: UNIPROT:O69736; EMBL:AF074611; NID:g3883003; PID:g3883035; PIDN:AA08
C;Genetics:
A;Gene: Y1035
A;Genome: plasmid pMT1

```

Query Match          10.7%; Score 71.5; DB 2; Length 220;
Best Local Similarity 20.1%; Pred. No. 9.6;
Matches 29; Conservative 28; Mismatches 66; Indels 21; Gaps 6;

Qy      1  MANKTMO-----PITSTANKIVV-SDPTRLSTFTFSASLLR-----QRVKVGIABLNNVSGQ 50
      : ||| : : : ||| : ||| : ||| : ||| : ||| :
Db      65  LVGKTVQLSAGITMSKSAADSFTTSDNDRVATVSGTGLVTGVTGPGVKITATDKQQLSA 124
      : ||| : : : ||| : ||| : ||| : ||| : ||| :
Qy      51  YVSIVYKPEPAKPECCADACVIMN-----ENQSIRTVISGSAENLATLKAEWETHKRNVD 105
      : ||| : : : ||| : ||| : ||| : ||| : ||| :
Db      125  SVEIVYKPV-----SVESIVTTPDSTSVKGGKVKLRVDVQPSNATNKKVTTWTSKNSDKA 179
      : ||| : : : ||| : ||| : ||| : ||| : ||| :
Qy      106  TLFASGN-AGLGFLDPTAAIVSSD 128
      : ||| : ||| : ||| : ||| : ||| : ||| :
Db      180  TVDQNGNVAGVAGTATIEVVSQD 203
      : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 12
JQ1674
protein kinase TMK1 (EC 2.7.1.1-), receptor type precursor - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1674

```

R;Chang, C.; Schaller, G.E.; Patterson, S.E.; Kwok, S.F.; Meyerowitz, E.M.; Bleecker, A. Plant Cell 4, 1263-1271, 1992

A:Title: The TWK1 gene from Arabidopsis codes for a protein with structural and biochemical properties similar to those of the mammalian protein tyrosine kinase

A:Reference number: JQ1674; PMID:93076110; PMID:1332795

A:Accession: JQ1674

A:Molecule type: DNA

A:Residues: 1-942 <CHN>

A:Cross-references: UNIPROT:P43298; GB:L00670; NID:gl66887; PIDN:AAA32876.1; PID:gl66888

C:Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology; p13

C:Keywords: ATP; autophosphorylation; glycoprotein; phosphotransferase; receptor; serine/

E:1-22/Domain: signal sequence #status predicted <SIG>

F:1-23-942/Product: protein kinase TWK1 #status predicted <MAT>

F:65-88/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>

F:89-111/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>

F:112-135/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>

F:136-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>

F:161-186/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>

F:187-209/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

F:210-232/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>

F:233-255/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>

F:256-279/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>

F:280-299/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>

F:300-322/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>

F:324-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>

F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>

F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>

F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F:480-503/Domain: transmembrane #status predicted <TM>

F:586-872/Domain: protein kinase homology <KIN>

F:594-602/Region: protein kinase ATP-binding motif

F:86,99,158,164,171,363,533,587/Binding site: carboxyhydrate (Asn) (covalent) #status predicted

F:616,634,717,719/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 10.7%; Score 71.5; DB 1; Length 942;

Best Local Similarity 23.6%; Pred. No. 56;

Matches 38; Conservative 26; Mismatches 38; Indels 59; Gaps 11;

Qy 4 KTMOPITSTANKIVMSDP-----TRLSTTFGASLLRQVRKVG-----IAEL 44

Db 37 KSLNPPSSFG-----WSDPDCKWTHIVCTGTRV--TRIQHGSLQGTLSPLDLNLSL 90

Qy 45 -----NNVSGQVSVYKRPAPKEGCACVIMPNENQSI RTVIGSGAENLAKA-- 95

Db 91 ERLELQWNNISG-----PVPSSLGLASLQVLMLS-NNNFDSPSDVFQGLTSLQSVE 141

Qy 96 -----EWETHK--RNVDTL--FASGNAGL-----GFLDP 120

Db 142 IDNNPFKSWEPESILRNASALQNFANSANVSGSLPGFLGP 182

RESULT 13

S38149

SIS2 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YKR072c

C:Species: Saccharomyces cerevisiae

C:Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004

C:Accession: S38149; S54982; S43078

R:Pohl, T.M.; Pohl, F.M.

submitted to the Protein Sequence Database, March 1994

A:Reference number: S37897

A:Accession: S38149

A:Molecule type: DNA

A:Residues: 1-562 <POH>

A:Cross-references: UNIPROT:P36024; EMBL:Z28297; NID:g486544; PID:g486545; MIPS:YKR072c

A:Experimental source: strain S288C

R:di Como, C.J.; Bose, R.; Arndt, K.T.

Genetics 139, 95-107, 1995

A:Title: Overexpression of SIS2, which contains an extremely acidic region, increases the

A:Reference number: S54982; PMID:95220693; PMID:7705654

A:Accession: S54982

A:Molecule type: DNA

A:Residues: 1-562 <DIW>

A:Cross-references: EMBL:U01878; NID:q430983; PIDN:AAA80000.1; PID:q430984

C;Genetics:

A;Gene: SGD:SIS2

A;Cross-references: SGD:S0001780; MIPS:YKR072c

A;Map position: 11R

C;Keywords: nucleus

Query Match 10.7%; Score 71; DB 2; Length 562;

Best Local Similarity 23.7%; Pred. No. 34;

Matches 27; Conservative 23; Mismatches 52; Indels 12; Gaps 4;

Qy 4 KTMQPISTANKIIVSDP-----TRLSTTFSSALLRQKVKVIGIAELNNVSGQYVSVYKRP 59

Db 68 KSIWNAATGTCGAVVNTPEGLKVPVATFSDLKQQKQSLTQLKNDSEKTSVPSNPA 127

Qy 60 KPKEGCADACVIMPNENQSIQRTV-IGSSAENLATLKAETHKRN-----VDTL 107

Db 128 PVSNSIPGNHAVIPNHTNTSKTTLQSGSP--LVNEMKDYDPKKDSALKIVDTM 179

RESULT 14

A86229

hypothetical protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: A86229

R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A86229

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-414 <STO>

A;Cross-references: UNIPROT:Q9SAV9; GB:A8005172; NID:g3482929; PIDN:AAC33214.1; GSPDB:GN

C;Genetics:

C;Superfamily: petunia myb-related protein 1; myb DNA-binding repeat homology

Query Match 10.6%; Score 70.5; DB 2; Length 414;

Best Local Similarity 21.9%; Pred. No. 26;

Matches 30; Conservative 20; Mismatches 68; Indels 19; Gaps 4;

Qy 3 NKTMQPISTANKIIVSDPTRLSTTFSSALLRQKVKVIGIAELNNVS-----GQY 51

Db 153 HKFSFSSSATNQDFLEPSPDLSYFGFKLFNSNLGLSVTTDSLSLCSMIPQFSPGNM 212

Qy 52 V-SVYKRPAPKEGCADACVIMPNENQSIQRTVIGSSAENLATLKAETHKRNVDTLFAS 110

Db 213 VGSVLQTPV-----CVKPSISLPPDNNSSSPISGGDHVKLAAPNWFQPTNNNTSNFF-- 265

Qy 111 GNAGLGFLDPTAAIVSS 127

Db 266 DNGGFSWSIPNSTSS 282

RESULT 15

JG0022

flagellar basal-body M-ring protein flif - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004

C;Accession: JG00022; A42365; B69624; S14494

R;Zuberi, A.R.; Ying, C.; Bischoff, D.S.; Ordal, G.W.

Gene 101, 23-31, 1991

A;Title: Gene-protein relationships in the flagellar hook-basal body complex of Bacillus subtilis.

A;Reference number: JG0019; MUID:91285431; PMID:1905667

A;Accession: JG0022

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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:38:08 ; Search time 91 Seconds
(without alignments)
497.627 Million cell updates/sec

Title: US-10-617-876-3

Perfect score: 666

Sequence: 1 MANKTQPIITSTANKIWSDDT.....NAGLGFLDPTAAIVSSDTTA 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	100.0	131	14	US-10-243-739-81 Sequence 81, Appl
2	666	100.0	131	14	US-10-244-065-81 Sequence 81, Appl
3	666	100.0	131	14	US-10-289-454-81 Sequence 81, Appl
4	666	100.0	131	15	US-10-346-190-96 Sequence 96, Appl
5	666	100.0	131	15	US-10-465-811-93 Sequence 93, Appl
6	666	100.0	131	15	US-10-289-456-113 Sequence 113, Appl
7	666	100.0	131	15	US-10-622-064-18 Sequence 18, Appl
8	666	100.0	131	15	US-10-617-876-3 Sequence 3, Appl
9	666	100.0	131	15	US-10-622-124-29 Sequence 29, Appl
10	666	100.0	131	16	US-10-622-087-29 Sequence 29, Appl
11	660	99.1	131	14	US-10-243-739-80 Sequence 80, Appl
12	660	99.1	131	14	US-10-244-065-80 Sequence 80, Appl
13	660	99.1	131	14	US-10-289-454-80 Sequence 80, Appl

14	660	99.1	131	15	US-10-346-190-95	Sequence 95, Appl
15	660	99.1	131	15	US-10-465-811-90	Sequence 90, Appl
16	660	99.1	131	15	US-10-289-456-112	Sequence 112, Appl
17	660	99.1	131	15	US-10-622-064-14	Sequence 14, Appl
18	660	99.1	131	15	US-10-617-876-1	Sequence 1, Appl
19	660	99.1	131	15	US-10-622-124-28	Sequence 28, Appl
20	660	99.1	131	16	US-10-622-087-28	Sequence 28, Appl
21	83.5	12.5	1619	16	US-10-437-963-121378	Sequence 121378,
22	81.5	12.2	662	16	US-10-437-963-121381	Sequence 121381,
23	81.5	12.2	1163	16	US-10-437-963-121376	Sequence 121376,
24	80	12.0	194	14	US-10-080-170-161	Sequence 161, App
25	80	12.0	194	16	US-10-080-170-161	Sequence 161, App
26	80	12.0	194	16	US-10-468-358-161	Sequence 161, App
27	79	11.9	329	16	US-10-755-889-426	Sequence 426, App
28	79	11.9	332	9	US-09-313-942-10	Sequence 10, Appl
29	79	11.9	332	9	US-09-935-868-10	Sequence 10, Appl
30	79	11.9	332	14	US-10-287-035-10	Sequence 10, Appl
31	79	11.9	332	14	US-10-282-162-10	Sequence 10, Appl
32	79	11.9	488	13	US-10-079-625-5	Sequence 5, Appl
33	79	11.9	708	14	US-10-313-135-2	Sequence 2, Appl
34	79	11.9	807	15	US-10-311-473-12	Sequence 12, Appl
35	79	11.9	859	9	US-09-313-942-7	Sequence 7, Appl
36	79	11.9	859	9	US-09-935-868-7	Sequence 7, Appl
37	79	11.9	859	14	US-10-287-035-7	Sequence 7, Appl
38	79	11.9	859	14	US-10-282-162-7	Sequence 7, Appl
39	79	11.9	918	10	US-09-853-180-4	Sequence 4, Appl
40	79	11.9	918	10	US-09-972-708-8	Sequence 8, Appl
41	79	11.9	918	14	US-10-177-293-230	Sequence 230, App
42	79	11.9	918	15	US-10-295-027-74	Sequence 74, Appl
43	79	11.9	918	15	US-10-058-270A-32	Sequence 32, Appl
44	79	11.9	918	16	US-10-715-667-8	Sequence 8, Appl
45	79	11.9	918	17	US-10-850-270-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-10-243-739-81
; Sequence 81, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Stornio, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-243-739-81

Query Match 100.0%; Score 666; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTQPIITSTANKIWSDDPTLSTTFSASLRQVRKVGIAELNNVSGYVSVKRPAP 60

Db 1 MANKTQPIITSTANKIWSDDPTLSTTFSASLRQVRKVGIAELNNVSGYVSVKRPAP 60

QY 61 KPGCCADACVIMPENQSIPTVSSAENLATLKAWEHTRKRVNVDTLFASGNAGLGFLDP 120

Db 61 KPGCCADACVIMPENQSIPTVSSAENLATLKAWEHTRKRVNVDTLFASGNAGLGFLDP 120

QY	121	TAAIVSSDTTA 131
Db	121	TAAIVSSDTTA 131
RESULT 2		
US-10-244-065-81		
; Sequence 81, Application US/10244065		
; Publication No. US20030996681		
; GENERAL INFORMATION:		
; APPLICANT: Bachmann, Martin F.		
; APPLICANT: Stornl, Tazio		
; APPLICANT: Maurer, Patrick		
; APPLICANT: Tissot, Alain		
; APPLICANT: Schwarz, Katrin		
; APPLICANT: Meijerink, Edwin		
; APPLICANT: Lipowsky, Gerard		
; APPLICANT: Pumpens, Paul		
; APPLICANT: Cielens, Indulis		
; APPLICANT: Renhofa, Regina		
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles		
; TITLE OF INVENTION: Method of Preparation and Use		
; FILE REFERENCE: 1700.0220001		
; CURRENT APPLICATION NUMBER: US/10/244,065		
; CURRENT FILING DATE: 2002-09-16		
; PRIOR APPLICATION NUMBER: 60/374,145		
; PRIOR FILING DATE: 2002-04-22		
; PRIOR APPLICATION NUMBER: 60/318,994		
; PRIOR FILING DATE: 2001-09-14		
; NUMBER OF SEQ ID NOS: 73		
; SOFTWARE: PatentIn version 3.1		
; SEQ ID NO 81		
; LENGTH: 131		
; TYPE: PRT		
; ORGANISM: Artificial Sequence		
; FEATURE:		
; OTHER INFORMATION: AP205 coat protein		
US-10-244-065-81		
Query Match 100.0%; Score 666; DB 14; Length 131;		
Best Local Similarity 100.0%; Pred. No. 3.6e-71;		
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MANKTMOPIITSTANKI VMSDPTRLSTTFSSALLRQRVKVGIAELNNVSGGYVSYYKRPAP 60
Db	1	MANKTMOPIITSTANKI VMSDPTRLSTTFSSALLRQRVKVGIAELNNVSGGYVSYYKRPAP 60
QY	61	KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFAFASGNAGLGFLDP 120
Db	61	KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFAFASGNAGLGFLDP 120
QY	121	TAAIVSSDTTA 131
Db	121	TAAIVSSDTTA 131
RESULT 3		
US-10-289-454-81		
; Sequence 81, Application US/10289454		
; Publication No. US20030157479A1		
; GENERAL INFORMATION:		
; APPLICANT: Bachmann, Martin		
; APPLICANT: Jennings, Gary		
; APPLICANT: Sonderegger, Ivo		
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases		
; FILE REFERENCE: 1700.0360001		
; CURRENT APPLICATION NUMBER: US/10/289,454		
; CURRENT FILING DATE: 2003-02-10		
; PRIOR APPLICATION NUMBER: US 60/396,636		
; PRIOR FILING DATE: 2002-07-19		
; PRIOR APPLICATION NUMBER: PCT/IB02/00166		
; PRIOR FILING DATE: 2002-01-21		


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QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 5
US-10-465-811-93
; Sequence 93, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; TITLE OF INVENTION: METHOD OF PREPARATION AND USE
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage AP205 mutant
US-10-465-811-93

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTWPITSTANKIVMSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKTWPITSTANKIVMSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 6
US-10-289-456-113
; Sequence 113, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-289-456-113

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTWPITSTANKIVMSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKTWPITSTANKIVMSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 7
US-10-622-064-18
; Sequence 18, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurer, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacteriophage AP205 mutant
US-10-622-064-18

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTWPITSTANKIVMSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKTWPITSTANKIVMSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 8
US-10-617-876-3
; Sequence 3, Application US/10617876
; Publication No. US20040076611A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tissot, Alain
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Molecular Antigen Arrays
; FILE REFERENCE: 1700.0310001
US-10-617-876-3

Query Match 100.0%; Score 666; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.6e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKTWPITSTANKIVMSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKTWPITSTANKIVMSDPTRLSTTFSASLLRQVRKVGVIAELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIPTVIGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
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Qy	1	MANKTQBITSTANKI	WSDPRLSTTTSS	LLRQVKV	GIAELNNV	SCQYVS	VYKRPAP	60
Db	1	MANKPMQPIITSTANKI	WSDPRLSTTTSS	LLRQVKV	GIAELNNV	SCQYVS	VYKRPAP	60
Qy	61	KPEGCADCACVIMPNENQ	SIRTVISGSAENL	ATLKAETHKKNVD	TLFASGNAGLGF	FLDP		120
Db	61	KPEGCADCACVIMPNENQ	SIRTVISGSAENL	ATLKAETHKKNVD	TLFASGNAGLGF	FLDP		120

RESULT 12
 US-10-244-065-80
 ; Sequence 80, Application US/10244065
 ; Publication No. US2003009968A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin F.
 ; APPLICANT: Storni, Tazio
 ; APPLICANT: Maurer, Patrick
 ; APPLICANT: Tissot, Alain
 ; APPLICANT: Schwarz, Katrin
 ; APPLICANT: Meijerink, Edwin
 ; APPLICANT: Lipowsky, Gerard
 ; APPLICANT: Pumpens, Paul
 ; APPLICANT: Cielens, Indulis
 ; APPLICANT: Renhofa, Regina
 ; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
 ; FILE REFERENCE: 1700.0220001
 ; CURRENT APPLICATION NUMBER: US/10/244,065
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 60/374,145
 ; PRIOR FILING DATE: 2002-04-22
 ; PRIOR APPLICATION NUMBER: 60/318,994
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 80
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: AP205 coat protein
 US-10-244-065-80

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RESULT 13
US-10-289-454-80
; Sequence 80, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderogger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases

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? FILE REFERENCE: 1700_0360001
? CURRENT APPLICATION NUMBER: US/10/289,454
? CURRENT FILING DATE: 2003-02-10
? PRIOR APPLICATION NUMBER: US 60/396,636
? PRIOR FILING DATE: 2002-07-19
? PRIOR APPLICATION NUMBER: PCT/IB02/00166
? PRIOR FILING DATE: 2002-01-21
? PRIOR APPLICATION NUMBER: US 10/050,902
? PRIOR FILING DATE: 2002-01-18
? PRIOR APPLICATION NUMBER: US 60/331,045
? PRIOR FILING DATE: 2001-11-07
? NUMBER OF SEQ ID NOS: 396
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 80
? LENGTH: 131
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Ap205 coat protein
? US-10-289-454-80

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RESULT 14
 US-10-346-190-95
 ; Sequence 95, Application US/10346190
 ; Publication No. US20030219459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bachmann, Martin
 ; APPLICANT: Maurex, Patrick
 ; APPLICANT: Pelliccioli, Erica
 ; APPLICANT: Renner, Wolfgang A.
 ; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
 ; FILE REFERENCE: 1700.0290003
 ; CURRENT APPLICATION NUMBER: US/10/346,190
 ; CURRENT FILING DATE: 2003-01-17
 ; PRIOR APPLICATION NUMBER: 60/396,590
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/393,725
 ; PRIOR FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 60/389,898
 ; PRIOR FILING DATE: 2002-06-20
 ; PRIOR APPLICATION NUMBER: PCT/IB02/00166
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: 10/050,902
 ; PRIOR FILING DATE: 2002-01-18
 ; NUMBER OF SEQ ID NOS: 164
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 95
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: RNA-phage AP205
 US-10-346-190-95

Query Match	99.1%	Score 660;	DB 15;	Length 131;
Best Local Similarity	99.2%	Pred. No. 1.9e-70;		
Matches 130;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

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Qy 1 MANKMQPITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKMQPITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Qy 61 KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
Db 61 KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

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RESULT 15
US-10-465-811-90
; Sequence 90, Application US/10465811
; Publication No. US20040005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; FILE REFERENCE: 1700.0290004
; CURRENT FILING DATE: 2003-06-20
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 90
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-465-811-90

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Query Match 99.1%; Score 660; DB 15; Length 131;
Best Local Similarity 99.2%; Pred. No. 1.9e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MANKMQPITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKMQPITSTANKIIVMSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Qy 61 KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
Db 61 KPGCADACVIMPNENOSIRTVISGSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

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Search completed: June 1, 2005, 09:51:00
Job time : 92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2005, 09:35:42 ; Search time 30 Seconds
(without alignments)
325.968 Million cell updates/sec

Title: US-10-617-876-3

Perfect score: 666

Sequence: 1 MANKTWPQTSTANKIWSKD.....NAGLGLDPTAAIVSSDTTA 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB pep.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB pep.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB pep.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB pep.*
- 5: /cgn2_6/prodata/1/iaa/6C COMB pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	11.9	332	4	US-09-313-942-10
2	79	11.9	488	2	US-08-599-455B-5
3	79	11.9	488	3	US-09-069-781B-5
4	79	11.9	488	3	US-09-137-132-5
5	79	11.9	488	3	US-08-864-564A-5
6	79	11.9	488	4	US-09-094-410-5
7	79	11.9	488	4	US-08-708-123D-5
8	79	11.9	488	4	US-08-583-153A-5
9	79	11.9	488	4	US-08-638-524B-5
10	79	11.9	658	2	US-08-825-558-4
11	79	11.9	658	3	US-09-312-611-4
12	79	11.9	708	1	US-07-797-556-2
13	79	11.9	708	1	US-08-308-881-2
14	79	11.9	708	2	US-09-058-263-2
15	79	11.9	708	2	US-09-059-099-2
16	79	11.9	708	3	US-09-058-264-2
17	79	11.9	708	4	US-09-455-962-2
18	79	11.9	708	5	PCT-US95-06530-2
19	79	11.9	859	4	US-09-313-942-7
20	79	11.9	918	2	US-08-825-558-6
21	79	11.9	918	3	US-09-312-611-6
22	79	11.9	918	4	US-09-853-180B-3
23	79	11.9	951	4	US-09-313-942-9
24	79	11.9	1158	4	US-09-313-942-26
25	79	11.9	1168	4	US-09-313-942-24
26	79	11.0	488	4	US-09-252-991A-28535
27	72	10.8	185	4	US-09-252-991A-31599

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28 70.5 10.6 248 4 US-09-252-991A-20247 Sequence 20247, A
29 70.5 10.6 5087 3 US-09-144-085-1 Sequence 1, Appli
30 70.5 10.6 6095 3 US-09-144-085-2 Sequence 2, Appli
31 70 10.5 179 4 US-09-270-767-43725 Sequence 43725, A
32 70 10.5 520 4 US-09-461-325-144 Sequence 144, App
33 70 10.5 520 4 US-10-012-542-144 Sequence 144, App
34 70 10.5 520 4 US-10-115-123-144 Sequence 144, App
35 69 10.4 414 4 US-09-489-039A-13320 Sequence 13320, A
36 67.5 10.1 300 4 US-09-252-991A-19422 Sequence 19422, A
37 67.5 10.1 343 3 US-08-858-003-32 Sequence 32, Appli
38 67.5 10.1 343 3 US-09-078-166-32 Sequence 32, Appli
39 67.5 10.1 343 3 US-08-997-467-32 Sequence 32, Appli
40 67 10.1 707 4 US-09-021-560-4 Sequence 4, Appli
41 67 10.1 707 4 US-09-202-178A-4 Sequence 4, Appli
42 66.5 10.0 480 4 US-09-710-279-2852 Sequence 2852, Ap
43 66.5 10.0 480 4 US-09-710-279-2986 Sequence 2986, Ap
44 66.5 10.0 490 3 US-09-134-001C-4019 Sequence 4019, Ap
45 66 9.9 287 4 US-09-292-858B-25 Sequence 25, Appli

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ALIGNMENTS

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RESULT 1
US-09-313-942-10
; Sequence 10, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-10

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Query Match 11.9%; Score 79; DB 4; Length 332;
Best Local Similarity 25.5%; Pred. No. 0.35;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIYMSDPTRLSTTFSASLLR-ORVKVGIAELNNVSGQYVSVYKRPAPKPGCAD 67
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Db 82 INRTASSVFTDIASLNILTCNLTFGLEQNVYGITISG-----LPPEKPKNL-- 132
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 68 ACVIMPNQSTRTVISGSAENLA-----TLKAEWETHK 101
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 133 SCIV--NEGKQRCWGDGGRETHLETFTLKSEWATHK 168
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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RESULT 2
US-08-599-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street

```

```
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-599-455B-5

Query Match 11.9%; Score 79; DB 2; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.62;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVNSDPTRLSTTFSSASLLR-ORVKVGIAELNNVSGQVSVYKRPAPKPECCAD 67
Db 53 INRTASSVTFTDIASLNQLTNCNLTFTGQLEQNVYGITIISG-----LPPEKPKNL-- 103

QY 68 ACVIMPNENOSIRTVISGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCWDGGRHLETNFTLKSEWATHK 139

RESULT 3
US-09-069-781B-5
; Sequence 5, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-781B-5

Query Match 11.9%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.62;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVNSDPTRLSTTFSSASLLR-ORVKVGIAELNNVSGQVSVYKRPAPKPECCAD 67
Db 53 INRTASSVTFTDIASLNQLTNCNLTFTGQLEQNVYGITIISG-----LPPEKPKNL-- 103

QY 68 ACVIMPNENOSIRTVISGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCWDGGRHLETNFTLKSEWATHK 139

RESULT 4
US-09-137-132-5
; Sequence 5, Application US/09137132
; Patent No. 6380363
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
```

```

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,564A
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-864-564A-5

Query Match      11.9%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred.No. 0.62; Indels 16; Gaps 5;
Matches 25; Conservative 21; Mismatches 36;

QY   9 ITSTANKIWSPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVVYVRPAPKEGCAD 67
     ||| : : : | : : : : : : : : : : : : : : : : : : : : : : :
Db   53 INRTASSVTFTDIASINLTCTNLTFCGLQNYYGITIISG-----LPPEPKNL-- 103

QY   68 ACVIMPNENQSRITVIGSAENLA---TLKAETHK 101
     ||| : : : | : : : : : : : : : : : : : : : : : : : : : : :
Db   104 SCIV--NEGKGRCWDGGRETHLETNFTLKSEWATHK 139

RESULT 6
US-09-094-410-5
; Sequence 5, Application US/09094410
; Patent No. 6403552
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-137-132-5

Query Match      11.9%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred.No. 0.62; Indels 16; Gaps 5;
Matches 25; Conservative 21; Mismatches 36;

QY   9 ITSTANKIWSPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVVYVRPAPKEGCAD 67
     ||| : : : | : : : : : : : : : : : : : : : : : : : : : : :
Db   53 INRTASSVTFTDIASINLTCTNLTFCGLQNYYGITIISG-----LPPEPKNL-- 103

QY   68 ACVIMPNENQSRITVIGSAENLA---TLKAETHK 101
     ||| : : : | : : : : ~~~~~~ ||||
Db   104 SCIV--NEGKGRCWDGGRETHLETNFTLKSEWATHK 139

RESULT 5
US-08-864-564A-5
; Sequence 5, Application US/08864564A
; Patent No. 6395498
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
```



```

Best Local Similarity 25.5%; Pred.No. 0.98;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVMSDPTRLSTFTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
| | | | | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 82 INRTASVFTDASLNLIQTNCNLIIFGQLEQNQVYGITISG-----LPPEKPKNL-- 132
| | | | | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :

QY 68 ACVIMPNENOSIRTVISGSAENLA----TLKAEWETHK 101 *
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
Db 133 SCIV--NEGKKMRCWDGGRETHLETNFTLKSEWATHK 168

RESULT 12
US-07-797-556-2
; Sequence 2, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; TITLE OF INVENTION: Inhibitory Factor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-797-556-2

Query Match 11.9%; Score 79; DB 1; Length 708;
Best Local Similarity 25.5%; Pred.No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVMSDPTRLSTFTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
| | | | | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 82 INRTASVFTDASLNLIQTNCNLIIFGQLEQNQVYGITISG-----LPPEKPKNL-- 132
| | | | | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :

QY 68 ACVIMPNENOSIRTVISGSAENLA----TLKAEWETHK 101
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
Db 133 SCIV--NEGKKMRCWDGGRETHLETNFTLKSEWATHK 168

RESULT 13
US-08-308-881-2
; Sequence 2, Application US/08308881
; Patent No. 5783672
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M

```

```

CLASSIFICATION:
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US/08/308,881
  FILING DATE: 12-SEP-1994
  APPLICATION NUMBER: US 08/249,553
  FILING DATE: 26-MAY-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Seese, Kathryn A.
    REGISTRATION NUMBER: 32,172
    REFERENCE/DOCKET NUMBER: 2614-A
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (206) 587-0430
    TELEFAX: (206) 233-0644
    TELEX: 756822
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 708 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
US-09-058-263-2

Query Match      11.9%; Score 79; DB 2; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY      9 ITSTANKIVSPDTRLSTTFPSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPGSCAD 67
DB      82 INRTASSVTFDIASLNIQLTNCILTFGQLEQNQVYGITISG-----LPPKPKML-- 132
QY      68 ACVMPENQSIIRTVISGSAENLA-----TLKAEWETHK 101
DB      133 SCIV--NECKKRCEDWDGGRTHLETNFTLKSEWATHK 168

RESULT 15:
US-09-059-099-2
; Sequence 2, Application US/09059099
; Patent No. 5925740
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,099
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 708 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-059-099-2

Query Match      11.9%; Score 79; DB 2; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVWSDPTRLSTTFESALLR-ORVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db 82 INRTASVTFDIASLNQLTCNLTFCQLEQNVYGITIISG-----LPPEKPKNL-- 132

QY 68 ACVIMPENOSIRTVISGSAENLA----TLKAEWETHK 101
Db 133 SCIV--NEGKKMRCEWDGGRETHLETNFTLKSEWATHK 168

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Search completed: June 1, 2005, 09:47:52
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:31:22 ; Search time 114 Seconds
(without alignments)
444.435 Million cell updates/sec

Title: US-10-617-876-3

Perfect score: 666

Sequence: 1 MANKTQPTSTTRANKIWSDD.....NAGLGFLDPTAALVSSDTTA 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1_Geneseq_16Dec04:*
2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	100.0	131	6	ABR56509 AP205 coa
2	666	100.0	131	6	ABU09695 Bacteriop
3	666	100.0	131	6	ABR44612 AP205 coa
4	666	100.0	131	7	ADD24203 Bacteriop
5	666	100.0	131	7	ADJ82146 Protein f
6	666	100.0	131	7	ADK17202 AP3 prote
7	666	100.0	131	8	ADJ36392 Bacteriop
8	666	100.0	131	8	ADI40712 Bacteriop
9	666	100.0	131	8	ADJ67171 Bacteriop
10	666	100.0	131	8	ADK52205 Bacteriop
11	666	100.0	131	8	ADL98305 Mutant Ba
12	660	99.1	131	6	ABR56508 AP205 coa
13	660	99.1	131	6	ABU09694 Bacteriop
14	660	99.1	131	6	ABR44611 AP205 coa
15	660	99.1	131	7	ADD24202 Bacteriop
16	660	99.1	131	7	ADJ82145 Protein f
17	660	99.1	131	7	ADK17201 AP1 prote
18	660	99.1	131	8	ADJ36389 Bacteriop
19	660	99.1	131	8	ADI40710 Bacteriop
20	660	99.1	131	8	ADJ67170 Bacteriop
21	660	99.1	131	8	ADK52204 Bacteriop
22	660	99.1	131	8	ADL98301 Bacteriop
23	80	12.0	194	5	ABU05510 M. tuberc
24	79	11.9	329	2	AAW17859 Rheumatol
25	79	11.9	329	8	ADR14425 Human NF-

26	79	11.9	332	2	AAW70799	AAW70799 Human gp1
27	79	11.9	332	3	AAW92188	AAW92188 Human gp1
28	79	11.9	332	7	ABW02167	ABW02167 Human gp1
29	79	11.9	488	4	AAE12610	AAE12610 Human gp1
30	79	11.9	488	5	AAE23860	AAE23860 Human Ob
31	79	11.9	488	8	ADG62980	ADG62980 Human gp1
32	79	11.9	658	2	AAW94576	AAW94576 Human gp1
33	79	11.9	708	2	AAW37804	AAW37804 Human gp1
34	79	11.9	708	2	AAW95911	AAW95911 gp130 N-t
35	79	11.9	727	3	AAW92192	AAW92192 Human gp1
36	79	11.9	738	3	AAW92194	AAW92194 Human gp1
37	79	11.9	809	5	AAU75498	AAU75498 Human Int
38	79	11.9	859	2	AAW70796	AAW70796 Human gp1
39	79	11.9	859	3	AAW92184	AAW92184 Human gp1
40	79	11.9	859	7	ABW02164	ABW02164 Human gp1
41	79	11.9	918	2	AAW10545	AAW10545 Recombina
42	79	11.9	918	2	AAW46233	AAW46233 Human sol
43	79	11.9	918	2	AAW75368	AAW75368 Human gp1
44	79	11.9	918	3	AAW44694	AAW44694 Human gp1
45	79	11.9	918	5	ABJ05551	ABJ05551 Breast ca

ALIGNMENTS

RESULT 1

ABR56509

ID ABR56509 standard; protein; 131 AA.

XX AC ABR56509;

XX DT 28-JUL-2003 (first entry)

XX DE AP205 coat protein SEQ ID NO:81.

XX KW Antigen presenting cell; APC; immune response; virus like particle; VLP;

XX KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;

XX KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;

XX KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;

XX KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;

XX KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;

XX KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;

XX KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;

XX KW inflammatory autoimmune disease.

XX OS Synthetic.

XX PN WO2003024480-A2.

XX PD 27-MAR-2003.

XX PF 16-SEP-2002; 2002WO-IB004252.

XX PR 14-SEP-2001; 2001US-0318967P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PI Bachmann MF, Storni T, Lechner F;

XX DR WPI; 2003-363095/34.

XX A composition, useful for enhancing an immune response against an antigen

PT or a virus-like particle, enhancing anti-viral protection in an animal,

PT or immunizing or treating tumors or infectious diseases, e.g. viral

PT infections.

XX Disclosure; Page 240-241; 243pp; English.

PS The present invention describes a composition (C) for enhancing an immune

XX response against an antigen or a virus-like particle in an animal. (C)

CC comprises a virus-like particle (VLP) bound to at least one antigen, or a

CC VLP capable of being recognised by the immune system of the animal. Also

CC described: (1) enhancing an immune response against an antigen or a VLP

CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
 CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumours and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 131 AA;

Query Match 100.0%; Score 666; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTQPIITSTANKIIVSDPTLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 DB 1 MANKTQPIITSTANKIIVSDPTLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVSSGAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 DB 61 KPEGCADACVIMPNENQSIPTVSSGAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131
 RESULT 2
 ABU09695
 ID ABU09695 standard; protein; 131 AA.
 AC ABU09695;
 DT 03-JUL-2003 (first entry)
 XX Bacteriophage AP205 coat protein mutant.

XX Bacteriophage AP205; coat protein; hypotensive; cerebroprotective;
 KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
 KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
 KW renin-activated angiotensin system; hypertension; stroke; infarction;
 KW congestive heart failure; kidney failure; retinal haemorrhage; mutant;
 KW mutein.
 XX
 OS Bacteriophage AP205.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5
 FT /note= "Wild type Pro substituted by Thr"
 XX
 PN WO2003031466-A2.
 XX
 PD 17-APR-2003.
 XX
 PP 07-OCT-2002; 2002WO-EP011219.
 XX
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396637P.

XX (CVTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachmann M;
 XX
 PI
 XX WPI; 2003-430264/40.
 DR N-PSDB; ABX95524.
 XX
 PT New angiotensin peptide moiety carrier conjugate comprising a carrier and
 an angiotensin peptide moiety, useful for treating or preventing a
 disorder associated with renin-activated angiotensin, e.g. hypertension
 or infarction.
 PT
 XX
 PS Disclosure; Page 96; 97pp; English.
 XX
 CC The invention describes an angiotensin peptide moiety carrier conjugate
 comprising: (a) a carrier with at least one first attachment site; and
 CC (b) at least one angiotensin peptide moiety with at least one second
 CC attachment site. The angiotensin peptide conjugate and compositions
 CC comprising them are useful for immunising an animal against an
 CC angiotensin peptide, and for treating or preventing a physical disorder
 CC associated with renin-activated angiotensin system such as hypertension,
 CC stroke, infarction, congestive heart failure, kidney failure, and retinal
 CC haemorrhage. The conjugate is also useful for inducing immune responses,
 CC including producing antibodies. This is the amino acid sequence of a
 CC bacteriophage AP205 coat protein mutant based on the wild type sequence
 CC shown in ABU09694 and used in the preparation of the vaccine conjugates
 CC of the invention
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 666; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTQPIITSTANKIIVSDPTLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 DB 1 MANKTQPIITSTANKIIVSDPTLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVSSGAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 DB 61 KPEGCADACVIMPNENQSIPTVSSGAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131
 RESULT 3
 ABR44612
 ID ABR44612 standard; protein; 131 AA.
 XX
 AC ABR44612;
 XX
 DT 25-JUL-2003 (first entry)
 XX
 XX AP205 coat protein SEQ ID NO:81.
 XX
 KW Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 KW immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
 KW immune response; immunisation; allergy; tumour; breast cancer;
 KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
 XX
 OS Synthetic.
 XX
 PN WO2003024481-A2.
 XX
 PD 27-MAR-2003.
 XX
 PP 16-SEP-2002; 2002WO-IB004132.
 XX

PR 14-SEP-2001; 2001US-0318994P.
PR 22-APR-2002; 2002US-0374145P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (MAUR/) MAURER P.
PA (TISS/) TISSOT A.
PA (SCHW/) SCHWARZ K.
PA (MELJ/) MELJERINK E.
PA (LIPO/) LIPOWSKY G.
PA (PUMP/) PUMPENS P.
PA (CIEL/) CIELENS I.
PA (RENH/) RENHOFA R.
XX
XX Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
PI Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T;
XX
XX WPI; 2003-354564/33.
XX
XX New compositions comprising immunostimulatory substances packaged into
PT virus-like particles, useful as a vaccine for enhancing an immune
PT response in animals, e.g. for treating or preventing allergies, tumors or
PT viral infections.
XX
XX Disclosure; Page 319-320; 322pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response in an animal. (C) comprises a virus-like particle (VLP), and an
CC immunostimulatory substance. The immunostimulatory substance is bound to
CC the VLP. Also described: (1) enhancing an immune response in an animal by
CC introducing (C) into the animal; (2) producing (C) for enhancing an
CC immune response in an animal; (3) vaccines comprising (C) together with a
CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
CC treating an animal by: (a) administering the vaccine to the animal; (b)
CC priming a T cell response in the animal by administering the vaccine; or
CC (c) boosting a T cell response in the animal by administering the
CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
CC antibacterial activities. (1) can be used in vaccines for enhancing an
CC immune response in an animal, particularly a mammal or human.
CC Specifically, (C) is useful for enhancing a B cell response, a T cell
CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
CC comprising (C) can also be used for immunising or treating an animal,
CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
CC reptiles or fish. (C) is particularly useful in prophylactic or
CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 131 AA;
XX
XX Query Match 100.0%; Score 666; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-72;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP 60
DB 1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP 60
QY 61 KPFGCADCACVIMPNENQSIPTVIGSGAENLATLKAETHKRVNVDTLFASGNAGLGLDLP 120
DB 61 KPFGCADCACVIMPNENQSIPTVIGSGAENLATLKAETHKRVNVDTLFASGNAGLGLDLP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131
RESULT 4
ADD24203
ID ADD24203 standard; protein; 131 AA.
XX
AC ADD24203;
XX
XX 15-JAN-2004 (first entry)
XX Bacteriophage AP205 coat protein #2.
XX vaccine composition; virus-like particle; core particle;
XX first attachment site; antigen; antigenic determinant; prion protein;
XX PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
XX prion disease; Bovine Spongiform Encephalopathy; BSE;
XX Creutzfeldt-Jakob Disease; prion; AP205; coat protein.
XX Synthetic.
XX Bacteriophage AP205.
XX WO2003059386-A2.
XX
XX 24-JUL-2003.
XX
XX 17-JAN-2003; 2003WO-EP000460.
XX
XX 19-JAN-2002; 2002US-00050902.
XX 21-JAN-2002; 2002WO-IB000166.
XX 08-JUL-2002; 2002US-0393725P.
XX 18-JUL-2002; 2002US-0396590P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
XX WPI; 2003-598483/56.
XX N-PSDB; ADD24204.
XX
XX A vaccine composition for preventing or treating prion diseases (e.g.
XX Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
XX phage) and at least one prion protein or peptide bound to the virus-like
XX particle.
XX
XX Disclosure; SEQ ID NO 96; 246pp; English.
XX
XX This invention relates to a novel vaccine composition comprising a virus-
XX like or a core particle with at least one first attachment site and at
XX least one antigen or antigenic determinant that is a prion protein (PrP)
XX or its dimer, or a PrP peptide, the antigen or antigenic determinant
XX being bound to the virus-like or core particle. The vaccine of the
XX invention may have neuroprotective or antiinflammatory activity. The
XX composition is useful as a medicament or in manufacturing a medicament
XX for the treatment or prevention of prion diseases. The prion diseases may
XX include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
XX Disease. The present sequence is that of a mutant RNA-phage AP205 coat
XX protein which is related to the invention.
XX
XX Sequence 131 AA;
XX
XX Query Match 100.0%; Score 666; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-72;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP 60
DB 1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP 60
QY 61 KPFGCADCACVIMPNENQSIPTVIGSGAENLATLKAETHKRVNVDTLFASGNAGLGLDLP 120
DB 61 KPFGCADCACVIMPNENQSIPTVIGSGAENLATLKAETHKRVNVDTLFASGNAGLGLDLP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131
RESULT 5
ADD24146
ID ADJ82146 standard; protein; 131 AA.

XX AC ADJ82146;
 XX DT 06-MAY-2004 (first entry)
 XX DE Protein for RANKL antigen array to treat bone disease.
 XX KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
 XX KW bone disease; encephalopathy; immune system stimulation.
 XX OS Unidentified.
 XX PN WO2003039225-A2.
 XX PD 15-MAY-2003.
 XX PF 07-NOV-2002; 2002WO-EP012449.
 XX PR 07-NOV-2001; 2001US-0331045P.
 XX PR 18-JAN-2002; 2002US-00050902.
 XX PR 21-JAN-2002; 2002WO-IB000166.
 XX PR 19-JUL-2002; 2002US-0396635P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PI Bachmann M, Maurer P, Spohn G;
 XX DR WPI; 2003-441430/41.
 XX PT New compositions comprising a core particle and at least one antigen or
 XX PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
 XX PT of bone diseases, particularly mammalian encephalopathies.
 XX PS Disclosure; SEQ ID NO 113; 222pp; English.
 XX CC The invention relates to a composition comprising a core particle having
 CC at least one first attachment site, and at least one antigen or antigenic
 CC determinant having at least one second attachment site. The antigen or
 CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
 CC peptide. The second attachment site is (non-) naturally occurring with
 CC the antigen or antigenic determinant, and is capable of association to
 CC the first attachment site. The antigen or antigenic determinant and the
 CC core particle interact through the association to form an ordered and
 CC repetitive antigen array. The composition is useful as a medicament, or
 CC for the manufacture of a medicament for treating bone diseases. The
 CC composition is especially useful for as a vaccine for therapy or
 CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
 CC and for stimulating mammalian immune system. This sequence represents a
 CC protein of the invention.
 XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 666; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKTQPIITSTANKIIVSDPTLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 Db 1 MANKTQPIITSTANKIIVSDPTLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 Qy 61 KPEGCADACVIMPNENOSIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGFLDP 120
 Db 61 KPEGCADACVIMPNENOSIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGFLDP 120
 Qy 121 TAAIVSSDITTA 131
 Db 121 TAAIVSSDITTA 131
 RESULT 6
 ADK17202
 ID ADK17202 standard; protein; 131 AA.
 XX

AC ADK17202;
 XX DT 06-MAY-2004 (first entry)
 XX DE AP3 protein for repetitive antigen array.
 XX KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;
 XX KW interleukin; IL-5; IL-13; eotaxin; repetitive antigen array;
 XX KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
 XX OS Unidentified.
 XX PN WO2003040164-A2.
 XX PD 15-MAY-2003.
 XX PF 07-NOV-2002; 2002WO-EP012455.
 XX PR 07-NOV-2001; 2001US-0331045P.
 XX PR 18-JAN-2002; 2002US-00050902.
 XX PR 21-JAN-2002; 2002WO-IB000166.
 XX PR 19-JUL-2002; 2002US-0396636P.
 XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PI Bachmann M, Jennings G, Sonderegger I;
 XX DR WPI; 2003-441518/41.
 XX PT Composition comprising an ordered and repetitive antigen or antigenic
 XX PT determinant array, useful as a medicament, or for manufacturing a
 XX PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
 XX PT Hodgkin's lymphoma.
 XX PS Disclosure; SEQ ID NO 81; 245pp; English.
 XX CC The invention relates to a composition comprising a virus-like particle
 CC and at least one antigen, which is a protein or peptide of interleukin
 CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
 CC core particle with at least one first attachment site and at least one
 CC antigen with at least one second attachment site, where the antigen is a
 CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
 CC is an attachment site naturally or not naturally occurring with the
 CC antigen or antigenic determinant. The second attachment site is capable
 CC of association to the first attachment site, and where the antigen or
 CC antigenic determinant and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC compositions are useful as medicaments, or for manufacturing a medicament
 CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
 CC Hodgkin's lymphoma and related diseases. This sequence is used to
 CC generate the compound of the invention.
 XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 666; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MANKTQPIITSTANKIIVSDPTLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 Db 1 MANKTQPIITSTANKIIVSDPTLSTTFSASLLRQVRKVGIAELNNVSGQVSVYKRPAP 60
 Qy 61 KPEGCADACVIMPNENOSIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGFLDP 120
 Db 61 KPEGCADACVIMPNENOSIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGFLDP 120
 Qy 121 TAAIVSSDITTA 131
 Db 121 TAAIVSSDITTA 131
 RESULT 7
 ADJ36392

ID ADJ36392 standard; protein; 131 AA.
 AC ADJ36392;
 XX
 XX
 XX 22-APR-2004 (first entry)
 XX
 DE Bacteriophage AP205 coat protein virus-like particle PST mutant.
 XX
 XX antiallergic; cytostatic; virucide; immunostimulant; vaccine;
 KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
 KW chronic disease; chronic viral disease; bacteriophage AP205;
 KW coat protein; VLP; adjuvant; mutant; mutin.
 XX
 OS Bacteriophage AP205.
 XX
 XX WO2004000351-A1.
 PN
 XX
 XX 31-DEC-2003.
 PD
 XX
 XX 20-JUN-2003; 2003WO-EP006541.
 PF
 XX
 XX 20-JUN-2002; 2002US-0389898P.
 PR
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX
 XX Bachman MF, Renner WA;
 PI
 XX
 XX WPI; 2004-108361/11.
 DR
 XX
 XX New compositions comprising a virus-like particle (VLP), an
 PT immunostimulatory substance bound to the VLP, and an antigen mixed with
 PT the VLP, useful for enhancing immune response or for treating e.g. tumors
 PT or chronic viral diseases.
 XX
 XX Example 16; SEQ ID NO 93; 252pp; English.
 PS
 XX
 XX The invention describes a composition for enhancing an immune response in
 CC an animal comprising a virus-like particle, an immunostimulatory
 CC substance bound to the virus-like particle, and an antigen mixed with the
 CC virus-like particle. The composition or the vaccine is useful in the
 CC manufacture of a pharmaceutical for the treatment of a disorder or
 CC disease such as allergies, tumours, chronic diseases and chronic viral
 CC diseases. The composition is also useful for enhancing an immune response
 CC in an animal. This is the amino acid sequence of a bacteriophage AP205
 CC coat protein PST mutant, a modified virus like particle (VLP) that can be
 CC used in the adjuvant of the invention.
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 666; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTQPTITSTANKIWSDPTRLSTFTFSASLLRQKVGIAELNNVSGQYVSVKRPAP 60
 DB 1 MANKTQPTITSTANKIWSDPTRLSTFTFSASLLRQKVGIAELNNVSGQYVSVKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131
 RESULT 8
 ID ADI40712
 XX ADI40712 standard; protein; 131 AA.
 AC ADI40712;
 XX
 XX 22-APR-2004 (first entry)
 DT

XX Bacteriophage AP205 mutant coat protein SEQ ID NO:3.
 DE
 XX
 XX virus-like particle; bacteriophage AP205; coat protein; cytostatic;
 KW vaccine; gene therapy; cancer; allergy; asthma; mutant.
 KW
 XX
 OS Bacteriophage AP205.
 OS Synthetic.
 OS
 PN WO20040007538-A2.
 XX
 XX 22-JAN-2004.
 PD
 XX
 XX 14-JUL-2003; 2003WO-EP007572.
 PF
 XX
 XX 17-JUL-2002; 2002US-0396126P.
 PR
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX
 XX Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofa R;
 PI
 XX
 XX WPI; 2004-122882/12.
 DR
 XX N-PSDB; ADI40713, ADI40834.
 DR
 XX
 XX New virus-like particle, useful for preparing a composition for treating
 PT or preventing a disease e.g., cancer, allergy or asthma.
 PT
 XX
 XX Claim 1; SEQ ID NO 3; 170pp; English.
 PS
 XX
 XX The present invention describes a virus-like particle (I) which
 CC comprises: (a) a protein having the 131-amino acid sequence of
 CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710
 CC or ADI40712 respectively; or (b) a mutin of the protein of (a). Also
 CC described: (1) a mutin of the recombinant protein having the 131-amino
 CC acid sequence; (2) a vector for producing a AP205 virus like particle
 CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%
 CC identical to that of the sequence comprising 3635 or 3613 bp or producing
 CC a recombinant protein comprising a nucleotide sequence encoding a
 CC polypeptide fused to a protein; (3) a pharmaceutical composition
 CC comprising the composition and a carrier; (4) a process for producing a
 CC non-naturally occurring, ordered and repetitive antigen array; (5) a
 CC method of treating or preventing a disease, disorder or physiologic
 CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-
 CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and
 CC (8) a method of producing the virus-like particle. (I) has cytostatic
 CC activity, and can be used in vaccines, and in gene therapy. The virus-
 CC like particle is useful for preparing a composition for treating or
 CC preventing a disease e.g., cancer, allergy or asthma. The present
 CC sequence represents a mutant bacteriophage AP205 coat protein, which is
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 666; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2e-72;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKTQPTITSTANKIWSDPTRLSTFTFSASLLRQKVGIAELNNVSGQYVSVKRPAP 60
 DB 1 MANKTQPTITSTANKIWSDPTRLSTFTFSASLLRQKVGIAELNNVSGQYVSVKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131
 RESULT 9
 ID ADJ67171
 ADJ67171 standard; protein; 131 AA.

XX AC ADJ67171;
XX DT 06-MAY-2004 (first entry)
XX DE Bacteriophage AP205 P5T mutant coat protein for antigen display array.
XX KW anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
XX KW antigenic array.
XX OS Bacteriophage AP205.
XX PN WO2004009124-A2.
XX PD 29-JAN-2004.
XX PF 18-JUL-2003; 2003WO-EP007849.
XX PR 19-JUL-2002; 2002US-0396638P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PI Bachmann MF, Fulurija A;
XX PS WPI; 2004-132866/13.
XX PT New composition comprising a core particle having a first attachment site
XX PT and an antigen or antigenic determinant which is a ghrelin or ghrelin
XX PT peptide having a second attachment site, useful for treating obesity.
XX PS Disclosure; SEQ ID NO 29; 175pp; English.
XX CC The invention relates to a new composition comprising: (i) a core
XX CC particle with at least one first attachment site; and (ii) a core
XX CC antigen or antigenic determinant with at least one second attachment
XX CC site, where the antigen or antigenic determinant is ghrelin or a ghrelin
XX CC peptide, and where the second attachment site being consisting of an
XX CC attachment site not naturally occurring with the antigen or antigenic
XX CC determinant and an attachment site naturally occurring with the antigen
XX CC or antigenic determinant, where the second attachment site is capable of
XX CC association to the first attachment site, and where the ghrelin or a
XX CC ghrelin peptide and the core particle interact through the association to
XX CC form an ordered and repetitive antigen array. The composition is useful
XX CC for treating obesity. The repetitive array may form part of a phage or
XX CC bacterial display array. This peptide corresponds to a mutant
XX CC Bacteriophage AP205 coat protein (Pro 5 changed to Thr) which can be used as
XX CC part of the repetitive or antigenic array.
XX SQ Sequence 131 AA;
Query Match 100.0%; Score 666; DB 8; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-72;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANKTQPIITSTANKIIVWSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAP 60
DB 1 MANKTQPIITSTANKIIVWSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAP 60
QY 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
DB 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131
RESULT 10
ADK52205
ID ADK52205 standard; protein; 131 AA.
XX ADK52205;
XX

DT 20-MAY-2004 (first entry)
XX Bacteriophage AP205 coat protein mutant P5T.
XX DE neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
XX KW core particle; antigen array; Alzheimer's disease; RNA bacteriophage;
XX KW coat protein; mutant; mutein.
XX OS Bacteriophage AP205.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT Misc-difference 5 /note= "Wild type Pro substituted by Thr"
XX PN WO2004016282-A1.
XX PD 26-FEB-2004.
XX PF 18-JUL-2003; 2003WO-EP007864.
XX PR 19-JUL-2002; 2002US-0396639P.
XX PR 15-MAY-2003; 2003US-0470432P.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX PA (NOVS) NOVARTIS PHARMA AG.
XX PI Bachmann MF, Tissot A, Ortman R, Lueoend R, Staufenbiel M;
XX PI Frey P;
XX PS WPI; 2004-203731/19.
XX PT Composition comprising a core particle with at least one attachment site,
XX PT and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
XX PT such as Alzheimer's disease.
XX PS Example 1; SEQ ID NO 29; 184pp; English.
XX CC The invention describes a novel composition comprising a core particle
XX CC with at least one attachment site, and an antigenic amyloid beta 1-6
XX CC peptide. The new composition comprises: a core particle with at least one
XX CC first attachment site; and at least one antigen or antigenic determinant
XX CC with at least one second attachment site, where the antigen or antigenic
XX CC determinant is a Amyloid beta 1-6 peptide, and where the second
XX CC attachment site comprises: an attachment site not naturally occurring
XX CC with the antigen or antigenic determinant; or an attachment site
XX CC naturally occurring with the antigen or antigenic determinant. The second
XX CC attachment site is capable of association to the first attachment site
XX CC and the beta 1-6 peptide and the core particle interact through the
XX CC association to form an ordered and repetitive antigen array. The
XX CC composition is useful for the manufacture of a medicament for treating
XX CC Alzheimer's disease and related diseases. This is the amino acid sequence
XX CC of an assembly-competent RNA bacteriophage AP205 mutant coat protein that
XX CC can be used in the preparation of the compositions and vaccines of the
XX CC invention.
XX SQ Sequence 131 AA;
Query Match 100.0%; Score 666; DB 8; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-72;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANKTQPIITSTANKIIVWSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAP 60
DB 1 MANKTQPIITSTANKIIVWSDPTRLSTTFSSALLRQVRKVGIAELNNVSGQVSVYKRPAP 60
QY 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
DB 61 KPEGCADACVIMPNENQSIPTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131

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RESULT 11
ADL98305
ID ADL98305 standard; protein; 131 AA.
XX
XX
AC ADL98305;
XX
XX
DT 19-NOV-2004 (first entry)
XX
DE Mutant Bacteriophage AP205 coat protein.
XX
XX haptan-carrier conjugate; recombinant virus protein; attachment site;
KW drug addition; fentanyl; heroin; morphine; amphetamine; cocaine;
KW methylenedioxymethamphetamine; methamphetamine; methylphenidate;
KW nicotine; cocaine; nornicotine; PCP; LSD; mescaline; psilocybin;
KW tetrahydrocannabinol; diazepam; desipramine; imipramine; nortriptyline;
KW amitriptyline; coat protein; mutant; muten.
XX
XX Bacteriophage AP205.
OS Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 5 /note= "Wild type Pro replaced by Thr"
FT
FT
XX
XX WO2004009116-A2.
XX
XX 29-JAN-2004.
XX
XX 18-JUL-2003; 2003WO-EP007850.
XX
XX 18-JUL-2002; 2002US-0396575P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann MF, Maurer P;
XX
XX WPI; 2004-132865/13.
XX
XX N-PSDB; ADL98306.
XX
XX
XX Haptan-carrier conjugate useful for treating or preventing addiction to
PT drug, comprises core particle having first attachment site and haptan
PT with second attachment site linked to form ordered and repetitive
PT conjugate.
XX
XX Example 9; SEQ ID NO 18; 144pp; English.
XX
XX The invention comprises a haptan-carrier conjugate consisting of a
CC carrier (e.g. a recombinant virus protein) that has at least one
CC attachment site, and at least one haptan with at least one second
CC attachment site. The method of the invention is useful for treating or
CC preventing addiction to a drug, such as: codeine, fentanyl, heroin,
CC morphine, amphetamine, cocaine, methylenedioxymethamphetamine,
CC methamphetamine, methylphenidate, nicotine, cotinine, nornicotine, PCP,
CC LSD, mescaline, psilocybin, tetrahydrocannabinol, diazepam, desipramine,
CC imipramine, nortriptyline and the amitriptyline class of drugs. The
CC method of the invention is also useful for preventing and treating
CC diseases associated with addiction. The present amino acid sequence was
CC used in an example of the invention.
XX
XX Sequence 131 AA;
SQ
Query Match 100.0%; Score 666; DB 8; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-72;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MANKTQPISTANKIWSDPTRLSTTFSSALLRQKVGIAELNNVSGQVSVYKRPAP 60
DB 1 MANKTQPISTANKIWSDPTRLSTTFSSALLRQKVGIAELNNVSGQVSVYKRPAP 60
QY 61 KPGGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

```

```

Db 61 KPGGCADACVIMPNENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131
RESULT 12
ABR56508
ID ABR56508 standard; protein; 131 AA.
XX
XX ABR56508;
XX
XX 28-JUL-2003 (first entry)
XX
XX AP205 coat protein SEQ ID NO:80.
XX
XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;
KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;
KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
KW inflammatory autoimmune disease.
XX
XX Synthetic.
XX
XX WO2003024480-A2.
XX
XX 27-MAR-2003.
XX
XX 16-SEP-2002; 2002WO-IB004252.
XX
XX 14-SEP-2001; 2001US-0318967P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann MF, Storni T, Lechner F;
XX
XX WPI; 2003-363095/34.
XX
XX A composition, useful for enhancing an immune response against an antigen
PT or a virus-like particle, enhancing anti-viral protection in an animal,
PT or immunizing or treating tumors or infectious diseases, e.g. viral
PT infections.
XX
XX Disclosure; Page 239-240; 243pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response against an antigen or a virus-like particle in an animal. (C)
CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
CC VLP capable of being recognised by the immune system of the animal. Also
CC described: (1) enhancing an immune response against an antigen or a VLP
CC in an animal comprising introducing (C) into the animal; (2) vaccines
CC comprising (C) together with a pharmaceutical diluent, carrier or
CC excipient; (3) immunising or treating an animal comprising administering
CC the vaccine to the animal, or priming or boosting a T cell response in
CC the animal by administering the vaccine; and (4) enhancing anti-viral
CC protection in an animal comprising introducing (C) into the animal. (C)
CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
CC antiallergic, immunosuppressive, antiaddictive, antiinflammatory,
CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
CC used for enhancing an immune response against an antigen or a VLP in an
CC animal, enhancing anti-viral protection in an animal, or immunising or
CC treating tumors and infectious diseases such as viral, bacterial,
CC parasitic or fungal infections. The vaccine compositions are also useful
CC for preventing or treating allergies, drug addiction, graft-versus-host
CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509

```

CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 131 AA;
Query Match 99.1%; Score 660; DB 6; Length 131;
Best Local Similarity 99.2%; Pred. No. 1.1e-71;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MANKTQPISTANKIWSDPTRLSTTFSSASLLRQVRKVGLAELNNVSGQVSVYKRPAP 60
DB 1 MANKPQPISTANKIWSDPTRLSTTFSSASLLRQVRKVGLAELNNVSGQVSVYKRPAP 60
QY 61 KPEGCADACVIMPENQSIKRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
DB 61 KPEGCADACVIMPENQSIKRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131
RESULT 13
ABU09694
ID ABU09694 standard; protein; 131 AA.
XX
AC ABU09694;
DT 03-JUL-2003 (first entry)
XX
DE Bacteriophage AP205 coat protein.
XX
KW Bacteriophage AP205; coat protein; hypotensive; cerebroprotective;
KW cardiant; nephrotropic; ophthalmological; immunostimulant; vaccine;
KW angiotensin peptide moiety carrier conjugate; angiotensin peptide;
KW renin-activated angiotensin system; hypertension; stroke; infarction;
KW congestive heart failure; kidney failure; retinal haemorrhage.
XX
OS Bacteriophage AP205.
XX
PN W02003031466-A2.
XX
PD 17-APR-2003.
XX
PF 07-OCT-2002; 2002WO-EP011219.
XX
PR 05-OCT-2001; 2001US-0326998P.
PR 07-NOV-2001; 2001US-0331045P.
PR 18-JAN-2002; 2002US-00050902.
PR 21-JAN-2002; 2002WO-IB000166.
PR 19-JUL-2002; 2002US-0396637P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M;
XX
XX WPI; 2003-430264/40.
DR N-PSDB; ABX95523.
DR
DR
XX New angiotensin peptide moiety carrier conjugate comprising a carrier and
PT an angiotensin peptide moiety, useful for treating or preventing a
PT disorder associated with renin-activated angiotensin, e.g. hypertension
PT or infarction.
XX
XX Disclosure; Page 96; 97pp; English.
PS
XX The invention describes an angiotensin peptide moiety carrier conjugate
CC comprising: (a) a carrier with at least one first attachment site; and
CC (b) at least one angiotensin peptide moiety with at least one second
CC attachment site. The angiotensin peptide moiety carrier conjugate and compositions
CC comprising them are useful for immunising an animal against an
CC angiotensin peptide, and for treating or preventing a physical disorder
CC associated with renin-activated angiotensin system such as hypertension,
CC stroke, infarction, congestive heart failure, kidney failure, and retinal

CC haemorrhage. The conjugate is also useful for inducing immune responses,
CC including producing antibodies. This is the amino acid sequence of a
CC bacteriophage AP205 coat protein used in the preparation of the vaccine
CC conjugates of the invention
XX
SQ Sequence 131 AA;
Query Match 99.1%; Score 660; DB 6; Length 131;
Best Local Similarity 99.2%; Pred. No. 1.1e-71;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MANKTQPISTANKIWSDPTRLSTTFSSASLLRQVRKVGLAELNNVSGQVSVYKRPAP 60
DB 1 MANKPQPISTANKIWSDPTRLSTTFSSASLLRQVRKVGLAELNNVSGQVSVYKRPAP 60
QY 61 KPEGCADACVIMPENQSIKRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
DB 61 KPEGCADACVIMPENQSIKRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
QY 121 TAAIVSSDTTA 131
DB 121 TAAIVSSDTTA 131
RESULT 14
ABR44611
ID ABR44611 standard; protein; 131 AA.
XX
AC ABR44611;
XX
DT 25-JUL-2003 (first entry)
XX
DE AP205 coat protein SEQ ID NO:80.
XX
KW Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
KW immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
KW immune response; leukaemia; allergy; tumour; breast cancer;
KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
XX
OS Synthetic.
XX
PN W02003024481-A2.
XX
PD 27-MAR-2003.
XX
PF 16-SEP-2002; 2002WO-IB004132.
XX
PR 14-SEP-2001; 2001US-0318994P.
PR 22-APR-2002; 2002US-0374145P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (MAUR/) MAURER P.
PA (TISS/) TISSOT A.
PA (SCHW/) SCHWARZ K.
PA (MEIJ/) MEIJERINK B.
PA (LIPO/) LIPOWSKY G.
PA (PUMP/) PUMPENS P.
PA (CIEL/) CIELENS I.
PA (RENH/) RENHOFA R.
XX
PI Maurer P, Tissot A, Schwarz K, Meijerink B, Lipowsky G;
PI Pumpens P, Cielens I, Renhofa R, Bachmann MF, Storni T;
XX
XX WPI; 2003-354564/33.
DR
XX New compositions comprising immunostimulatory substances packaged into
PT virus-like particles, useful as a vaccine for enhancing an immune
PT response in animals, e.g. for treating or preventing allergies, tumors or
PT viral infections.
XX
XX Disclosure; Page 319; 322pp; English.
PS

XX The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
 CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence 131 AA;

Query Match 99.1%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.1e-71;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKTQPTSTANKIWSDPTRLSTTFSASLLRQKVGIASLNNVSGQYVSVYKRPAP 60
 DB 1 MANKPQPTSTANKIWSDPTRLSTTFSASLLRQKVGIASLNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPENQSIQRTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPENQSIQRTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDFTA 131
 DB 121 TAAIVSSDFTA 131

RESULT 15
 ADD24202
 ID ADD24202 standard; protein; 131 AA.

XX ADD24202;

XX 15-JAN-2004 (first entry)

DE Bacteriophage AP205 coat protein #1.

XX vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion; AP205; coat protein.

XX Bacteriophage AP205.

XX WO2003059386-A2.

PD 24-JUL-2003.

XX 17-JAN-2003; 2003WO-EP000460.

XX 18-JAN-2002; 2002US-00050902.

PR 21-JAN-2002; 2002WO-IB000166.

PR 08-JUL-2002; 2002US-0393725P.

XX 18-JUL-2002; 2002US-0396590P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;

XX WPI; 2003-598483/56.

DR N-PSDB; ADD24201.

XX A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.

XX Disclosure; SEQ ID NO 95; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a RNA-phage AP205 coat protein
 CC which is related to the invention.

XX Sequence 131 AA;

Query Match 99.1%; Score 660; DB 7; Length 131;
 Best Local Similarity 99.2%; Pred. No. 1.1e-71;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKTQPTSTANKIWSDPTRLSTTFSASLLRQKVGIASLNNVSGQYVSVYKRPAP 60
 DB 1 MANKPQPTSTANKIWSDPTRLSTTFSASLLRQKVGIASLNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPENQSIQRTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 DB 61 KPEGCADACVIMPENQSIQRTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDFTA 131
 DB 121 TAAIVSSDFTA 131

Search completed: June 1, 2005, 09:41:59
 Job time : 114 secs

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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:34:57 ; Search time 24 Seconds
(without alignments)
525.183 Million cell updates/sec

Title: US-10-617-876-1
Perfect score: 668
Sequence: 1 MANKPMQPTSTANKIWS.....NAGLGFLDPTAIVSSDTTA 131

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	80	12.0	194	2 S72877	hypothetical prote
2	79	11.8	918	2 A36337	membrane glycoprot
3	78	11.7	305	2 A75334	lacyl-carrier-prot
4	76.5	11.5	546	2 B47073	chaperonin GroEL -
5	75.5	11.3	519	2 I45847	acetylcholine rece
6	73.5	11.0	213	2 D70972	probable enoyl-coA
7	73.5	11.0	291	2 T51668	myb-related transc
8	73.5	11.0	831	2 A11515	ORFA of Listeria s
9	73	10.9	547	2 AC1314	malolactic enzyme
10	72	10.8	273	2 B64446	formylmethanofuran
11	70.5	10.6	414	2 A86229	hypothetical prote
12	70.5	10.6	646	2 T17631	hypothetical prote
13	70.5	10.6	26926	1 I38344	titin, cardiac mus
14	70	10.5	519	2 I56566	nicotinic acetylch
15	70	10.5	519	2 S13874	nicotinic acetylch
16	69.5	10.4	319	2 T27862	hypothetical prote
17	69.5	10.4	358	2 S31407	(2'-5')oligo(A) sy
18	69.5	10.4	643	2 I50539	intermediate filam
19	69.5	10.4	942	1 JQ1674	protein kinase TMK
20	69.5	10.4	1078	2 T30860	trial protein - Sal
21	69	10.3	374	2 T10415	virus envelope pro
22	69	10.3	562	2 S38149	Sis2 protein - yea
23	69	10.3	666	2 S29349	hypothetical prote
24	69	10.3	2187	2 S60224	polyketide synthas
25	68	10.2	252	2 C69172	conserved hypotet
26	68	10.2	267	2 A97762	hypothetical prote
27	68	10.2	350	2 S51494	arabinogalactan en
28	67.5	10.1	330	2 T37854	probable IUNH-fam
29	67.5	10.1	577	2 H69354	probable fatty-aci

30	67.5	10.1	903	2 T09143	alpha-glucosidase
31	67.5	10.1	913	2 AC2445	hypothetical prote
32	67.5	10.1	1052	2 A10346	Acrl/Acrd/Acrf fam
33	67	10.0	143	2 T14664	hypothetical prote
34	67	10.0	220	2 T14951	hypothetical prote
35	67	10.0	398	2 E82262	hypothetical prote
36	67	10.0	454	2 S16522	mitosis-specific c
37	67	10.0	507	2 B84506	probable Athila re
38	67	10.0	701	2 S35313	TiPl protein - yea
39	67	10.0	772	1 A44052	outer layer protei
40	67	10.0	1056	2 T33167	hypothetical prote
41	67	10.0	1350	2 T30341	zinc finger protei
42	67	10.0	6805	2 S20901	titin - rabbit (fr
43	66.5	10.0	194	2 C86676	hypothetical prote
44	66.5	10.0	419	2 T36272	hypothetical prote
45	66.5	10.0	625	2 C25977	phosphotransferase

ALIGNMENTS

RESULT 1

S72877
hypothetical protein B2126_F3_115 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72877
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B2126.
A;Reference number: S72585
A;Accession: S72877
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <SMI>
A;Cross-references: UNIPROT:Q49803; EMBL:U00017; NID:g466994; PIDN:AAAL7217.1; PID:g467070;
C;Genetics:
A;Start codon: GTG

Query Match	12.0%;	Score 80;	DB 2;	Length 194;
Best Local Similarity	25.0%;	Pred. No. 1.1;		
Matches	30;	Conservative	10;	Mismatches 26; Indels 54; Gaps 6;
Qy	8	PTSTANKIWS--DPTRLSTTFESALLRQVRVKVIGIAELNNVSGQVSVYK-----RPAP 60		
Db	110	PMTFTANNIAWSKNPSDLATIS-----VNIAQTNN-----SVFSFPMFEPTFP 154		
Qy	61	KEGCGACACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGFLDP 120		
Db	155	PPQ-----QSQWLSKRTADMLEFGNSS-GLTNP 182		

RESULT 2

A36337
membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
C;Accession: A36337
R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A;Reference number: A36337; MUID:91084844; PMID:2261637
A;Accession: A36337
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-918 <HIB>
A;Cross-references: UNIPROT:P40189; GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
C;Genetics:
A;Gene: GDB:IL6ST; GP130
A;Cross-references: GDB:126725; OMIM:600694
A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
F;134-316/Domain: cytokine receptor homology <CRS>

A>Note: sequence extracted from NCBI backbone (NCBIN:126968, NCBIP:126970)
C;Superfamily: chaperonin groEL
C;Keywords: molecular chaperone

Query Match 11.5%; Score 76.5; DB 2; Length 546;
Best Local Similarity 20.7%; Pred. No. 8.9;
Matches 28; Conservative 25; Mismatches 65; Indels 17; Gaps 3

Qy 3 NKPMPITSTANKI--YMSDFRLSTFTFSASLLLRQRVKVGI AELN-----NVS 48
| | | | | : | | | | | : | | | | | : | | | | | :
Db 68 NMGAQMVEKVASKTSDIAGDGTATTTLVAQAAMVREGLKAAGAAMPMDLKRGMDKAVEAA 127
| | | | | : | | | | | : | | | | | : | | | | | :
Qy 49 GOYYSVVRRPAPKEGACADACVIMPNENQSIRTVISSAENL---ATLKAEWETHRNV 105
| | | | | : | | | | | : | | | | | : | | | | | :
Db 128 TEELKLKSLKPCPRPMALAQGVTTISANSDDSGTIIAEAMEKVREGVTIVEDGTSLONEL 187
| | | | | : | | | | | : | | | | | : | | | | | :
Qy 106 TLPFASGNAGLGFLDP 120
| | | | | : | | | | | : | | | | | :
Db 188 DVVEGMQFDRLSP 202
| | | | | : | | | | | : | | | | | :

RESULT 5
I45847
acetylcholine receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: I45847
R;Takai, T.; Noda, M.; Furutani, Y.; Takahashi, H.; Notake, M.; Shimizu, S.; Kato, J.
Eur. J. Biochem. 143, 109-115, 1984
A>Title: Primary structure of gamma subunit precursor of calf-muscle acetylcholine receptor
A;Reference number: I45847; MUID:84285374; PMID:6547904
A;Accession: I45847
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-519 <FA>
A;Cross-references: UNIPROT:P13536; GB:M28307; MID:g162601; PIDN:AAA30351.1; PDB:1ZM0
C;Genetics:
A;Gene: ACHR
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match 11.3%; Score 75.5; DB 2; Length 519;
Best Local Similarity 22.0%; Pred. No. 11;
Matches 37; Conservative 21; Mismatches 59; Indels 51; Gaps 6

Qy 4 KPMOPI-----TSPANKIVMSDPTRLSTFTFSASLLRQRVKVGIA-----EL 44
| | | | | : | | | | | : | | | | | : | | | | | :
Db 360 RPLAPVAVQDAHPRLONGSSGWPIITAGEVALCPRLSELLFRQRMGLVRAALEKLEK 419
| | | | | : | | | | | : | | | | | : | | | | | :
Qy 45 NNVSQG---YVSVYKRPAPKEGCADACVIMPNENQSIRTVISSAENLATLKAEWETHK 101
| | | | | : | | | | | : | | | | | : | | | | | :
Db 420 GPESGGSPWGCSLQAAPAQAICVEACNLRIARHQHTHFDSCN-----KEWFLVG 471
| | | | | : | | | | | : | | | | | : | | | | | :

Qy 102 RNVD-----TLFASGNAGLGLF-----DPTAAIVSSD 128
| | | | | : | | | | | : | | | | | : | | | | | :
Db 472 RVLDRCVCLAMLRLFVCGTAGIFLMAHYNRVPALPFPGDPRSILPSSD 519
| | | | | : | | | | | : | | | | | : | | | | | :

RESULT 6
D70972
probable enoyl-coA hydratase - Mycobacterium tuberculosis (strain H37Rv)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2004
C;Accession: D70972
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Holt,
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.;
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70972
A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-213 <COL>
A;Cross-references: UNIPROT:O50402; GB:AL009198; GB:AL123456; NID:G3242262; PIDN:CAA1579
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: echA18
C;Superfamily: Naphthoate synthase

Query Match 11.0%; Score 73.5; DB 2; Length 213;
Best Local Similarity 27.6%; Pred. No. 5.8;
Matches 24; Conservative 14; Mismatches 42; Indels 7; Gaps 3;
QY 33 LRORVKVGI AELNNVSGQYVSV---YKRPAPKPEGACACVIMPNENQSIQRTVIGSSAE 88
Db 1 MRRAMTKMD EASNPCCGDI EAECQMLMRQPPAEGVVDVRAQLQRHNVALLITLSHPQAQ 60
QY 89 NLATLKA EWEETHKRNVDTLFASGNAGL 115
Db 61 NALNL-ASWRLKRLDLDL--AGESGL 84

RESULT 7
T51668
myb-related transcription factor MYB61 [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51668
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
A;Reference number: 214349; MUID:9839469; PMID:9839469
A;Accession: T51668
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-291 <KRA>
A;Cross-references: UNIPROT:Q9SBP9; EMBL:AF062896; PIDN:AAC03618.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: MYB61
A;Map position: 1
C;Keywords: transcription factor

Query Match 11.0%; Score 73.5; DB 2; Length 291;
Best Local Similarity 23.0%; Pred. No. 8.4;
Matches 32; Conservative 19; Mismatches 67; Indels 21; Gaps 5;
QY 3 NKPMQPIITANK--IVWSDPTRLSTTFSASLLRQVRKVGI AELNNVS-----G 49
Db 76 NDHKSPSSSATNQDFFLERPSDLSYFGQKLFNLSGLSVTTDSSLCSMIPPQFSPG 135
QY 50 QYV-SVYKRPAPKPEGACACVIMPNENQSIQRTVIGSSAENLATLKA EWEETHKRNVDTLF 108
Db 136 NMVGSVLQTPV-----CVKPSISLPHDNNSSSIFSGDGHVKLAAPNWEFTNNNTSNPF 190
QY 109 ASGNAGLGLDPTAAIVSS 127
Db 191 --DNGGFSWSIPNSSSTSS 207

RESULT 8
A11515
ORF of *Listeria seeligeri*, (LPXTG motif) homolog lin0665 [imported] - *Listeria innocua*
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11515
R;Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11515
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-831 <GLA>
A;Cross-references: UNIPROT:Q92D26; GB:AL592022; PIDN:CAC95897.1; PID:gl6413105; GSPDB:C
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin0665

Query Match 11.0%; Score 73.5; DB 2; Length 831;
Best Local Similarity 25.8%; Pred. No. 30;
Matches 34; Conservative 18; Mismatches 53; Indels 27; Gaps 7;
QY 8 PITSTAN-KIVWSDPTRLSTTFSASLLRQVRKVGI AELNNVSGQ-----YVSVYKRPAP-- 60
Db 646 PLVSDMNDKVKWGPVGDYEVTLN-----VNEDGVA AEAKTFIVRLKSPAPII 694
QY 61 --KPEGACACVIMPNENQSIQRTVIGSSAENLATL-----KA EWEETHKRNVDTLFASGNA 113
Db 695 TVDPEVSYDSAIL-KNETELLKVRKTNDSAITSDAPDKVKWQTPGSGYTVTLNAVNE 753
QY 114 GLGFLDPTAAIV 125
Db 754 GIP-ADPVTIV 764

RESULT 9
AC1314
malolactic enzyme (malate dehydrogenase) homolog lmo1915 [imported] - *Listeria monocytogenes*
C;Species: *Listeria monocytogenes*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1314
R;Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <GLA>
A;Cross-references: UNIPROT:Q9YSY8; GB:NC_003210; PIDN:CAC99993.1; PID:gl64111368; GSPDB:C
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1915
C;Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 10.9%; Score 73; DB 2; Length 547;
Best Local Similarity 25.0%; Pred. No. 20;
Matches 33; Conservative 21; Mismatches 56; Indels 22; Gaps 4;
QY 12 TANKIVWSDPTRLSTTFSASLLRQVRKVGI AELNNVSGQYVSVYKRPAPK-----PEGC 65
Db 191 TNNETLLNDPLVYG-----NKRPLRSESEYDAFIASFVNVKVEFPKAILHWEDEGR 242
QY 66 ADACVIMPNENQSIQRTV-----ISGS-----AENLATLKA EWEETHKRNVDTLFASGNAGLGP 117
Db 243 ANASRIILNHYRDKICTFNDDIQGTGMVVAVALTIQVSRIPLSEQKIIFGAGTAGIGI 302
QY 118 LDPTAAIVSSDT 129
Db 303 ADQLSAQLMRET 314

RESULT 10
B64446
formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - *Methanococcus jannaschii*
C;Species: *Methanococcus jannaschii*
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004

A;Accession: I56566
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-519 <RES>
A;Cross-references: UNIPROT:P04760; GB:M30514; NID:g200012; PID:g200013
R;Yu, L.; LaPolla, R.J.; Davidson, N.
Nucleic Acids Res. 14, 3539-3555, 1986
A;Title: Mouse muscle nicotinic acetylcholine receptor gamma-subunit: cDNA sequence and
A;Reference number: A24919; MUID:86205253; PMID:3010242
A;Accession: A24919
A;Molecule type: mRNA
A;Residues: 1-230, 'V', 232-345, 'L', 347-519, 'X' <YUL>
A;Note: the authors translated the codon ATG for residue 116 as His
R;Gardner, P.D.; Heinemann, S.; Patrick, J.
Brain Res. Mol. Brain Res. 3, 69-76, 1987
A;Title: Transcriptional regulation of nicotinic acetylcholine receptor genes: identifier
A;Reference number: A43774
A;Accession: A43774
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <GAR>
A;Cross-references: GB:M27455; NID:g387692; PIDN:AAA70247.1; PID:g191613
R;Crowder, C.M.; Merlie, J.P.
Mol. Cell. Biol. 8, 5257-5267, 1988
A;Title: Stepwise activation of the mouse acetylcholine receptor delta- and gamma-subunit
A;Reference number: I49457; MUID:89218986; PMID:3244354
A;Accession: I49457
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-18 <RE2>
A;Cross-references: GB:M22391; NID:g191597; PIDN:AAA37152.1; PID:g553854
C;Genetics:
A;Intons: 19/1
A;Note: list of introns may be incomplete
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-519/Product: nicotinic acetylcholine receptor gamma chain #status predicted <MAT>

Query Match 10.5%; Score 70; DB 2; Length 519;
Best Local Similarity 25.7%; Pred. No. 38;
Matches 27; Conservative 14; Mismatches 38; Indels 26; Gaps 4;

Qy 29 SASLLRQVRKVGIAE-----LNN-----VSGQYVSVYKRPAPKPEGCADACVIMPNENQS 78
Db 397 SELLFRQRNGILVQAVLEKLENGPEVRSQEFQCSGLKQASPAIQACVDCNLMARARRQ 456

Qy 79 IRTVISSAENLATLKAETHKRNVD-----TLFASGNAGL 115
Db 457 QSHFDSGN-----BEWLVGRVLDRVCFIAMLSLFCGTAGI 493

RESULT 15
S13874
nicotinic acetylcholine receptor gamma chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S13874; S03082
R;Witzemann, V.; Stein, E.; Barg, B.; Konno, T.; Koenen, M.; Kues, W.; Criado, M.; Hofmar
Eur. J. Biochem. 194, 437-448, 1990
A;Title: Primary structure and functional expression of the alpha-, beta-, gamma-, delta
A;Reference number: S13872; MUID:91099317; PMID:1702709
A;Accession: S13874
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-519 <WIT>
A;Cross-references: UNIPROT:P19916; EMBL:X74834; NID:g398835; PIDN:CAA52828.1; PID:g39882
R;Witzemann, V.; Barg, B.; Nishikawa, Y.; Sakmann, B.; Numa, S.
FEBS Lett. 223, 104-112, 1987
A;Title: Differential regulation of muscle acetylcholine receptor gamma- and epsilon-subunit
A;Reference number: S03081; MUID:88030021; PMID:3666131
A;Accession: S03082
A;Molecule type: DNA

A;Residues: 203-306 <W12>
A;Cross-references: EMBL:X06364; NID:955588; PIDN:CAA29662.1; PID:955589
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
E;39-65/Domain: transmembrane #status predicted <TM1>
F;72-90/Domain: transmembrane #status predicted <TM2>

Query Match 10.5%; Score 70; DB 2; Length 519;
Best Local Similarity 25.8%; Pred. No. 38;
Matches 31; Conservative 13; Mismatches 46; Indels 30; Gaps 5;

Qy	18	WSDPTR----	LSSTFSASLLRQVRKVGIAE-----LNN-----VSGQYVSYYKRPAPKPE	63
Db	382	WPIMTREEGDLCPLPRSELLFRQQRNGLVQAVLEKLENGPEMRQSEFCGSLKQASPAIQ	441	
Qy	64	GCADACVIMPNENQSIKTVISGSAENLATLKAWEIHKRNVD-----TLFASGNAGL	115	
Db	442	ACVDACNLMARHQSHFDSGN-----EWWLLVGRVLDRCVFLAMLSLFCGTAGI	493	

Search completed: June 1, 2005, 09:46:47
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:38:08 ; Search time 91 Seconds
(without alignments)
497.627 Million cell updates/sec

Title: US-10-617-876-1
Perfect score: 668
Sequence: 1 MANKMPQITSTANKIWS...NAGLGFLDPTAAIVSSDTTA 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668	100.0	131	14	US-10-243-739-80
2	668	100.0	131	14	US-10-244-065-80
3	668	100.0	131	14	US-10-289-454-80
4	668	100.0	131	15	US-10-346-190-95
5	668	100.0	131	15	US-10-465-811-90
6	668	100.0	131	15	US-10-289-456-112
7	668	100.0	131	15	US-10-622-064-14
8	668	100.0	131	15	US-10-617-876-1
9	668	100.0	131	15	US-10-622-087-28
10	668	100.0	131	16	US-10-622-739-81
11	660	98.8	131	14	US-10-243-739-80
12	660	98.8	131	14	US-10-244-065-81
13	660	98.8	131	14	US-10-289-454-81

14	660	98.8	131	15	US-10-346-190-96	Sequence 96, Appl
15	660	98.8	131	15	US-10-465-811-93	Sequence 93, Appl
16	660	98.8	131	15	US-10-289-456-113	Sequence 113, Appl
17	660	98.8	131	15	US-10-622-064-18	Sequence 18, Appl
18	660	98.8	131	15	US-10-617-876-3	Sequence 3, Appl
19	660	98.8	131	15	US-10-622-124-29	Sequence 29, Appl
20	660	98.8	131	16	US-10-622-087-29	Sequence 29, Appl
21	83.5	12.5	1619	16	US-10-437-963-121378	Sequence 121378,
22	81.5	12.2	662	16	US-10-437-963-121381	Sequence 121381,
23	81.5	12.2	1163	16	US-10-437-963-121376	Sequence 121376,
24	80	12.0	194	14	US-10-080-170-161	Sequence 161, App
25	80	12.0	194	16	US-10-468-356-161	Sequence 161, App
26	80	12.0	194	16	US-10-468-356-161	Sequence 161, App
27	79	11.8	332	9	US-09-313-942-10	Sequence 426, App
28	79	11.8	332	9	US-09-313-942-10	Sequence 10, Appl
29	79	11.8	332	14	US-10-287-035-10	Sequence 10, Appl
30	79	11.8	332	14	US-10-287-035-10	Sequence 10, Appl
31	79	11.8	332	14	US-10-282-162-10	Sequence 5, Appl
32	79	11.8	488	13	US-10-079-625-5	Sequence 2, Appl
33	79	11.8	708	14	US-10-313-135-2	Sequence 12, Appl
34	79	11.8	807	15	US-10-311-473-12	Sequence 7, Appl
35	79	11.8	859	9	US-09-313-942-7	Sequence 7, Appl
36	79	11.8	859	9	US-09-313-942-7	Sequence 7, Appl
37	79	11.8	859	14	US-10-287-035-7	Sequence 7, Appl
38	79	11.8	859	14	US-10-282-162-7	Sequence 7, Appl
39	79	11.8	918	10	US-09-853-180-4	Sequence 4, Appl
40	79	11.8	918	10	US-09-972-708-8	Sequence 8, Appl
41	79	11.8	918	14	US-10-177-293-230	Sequence 230, App
42	79	11.8	918	15	US-10-295-027-74	Sequence 74, Appl
43	79	11.8	918	15	US-10-058-270A-32	Sequence 32, Appl
44	79	11.8	918	16	US-10-715-667-8	Sequence 8, Appl
45	79	11.8	918	17	US-10-850-270-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-10-243-739-80
; Sequence 80, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; FILE OF INVENTION: Immune Responses Induced by Virus Like Particles
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-243-739-80

Query Match	100.0%	Score 668;	DB 14;	Length 131;
Best Local Similarity	100.0%	Pred. No. 7.9e-71;	Indels 0;	Gaps 0;
Matches 131;	Conservative 0;	Mismatches 0;		
QY	1	MANKMPQITSTANKIWS	DTLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP	60
Db	1	MANKMPQITSTANKIWS	DTLSTTFSASLLRQKVGIAELNNVSGQVSVYKRPAP	60
QY	61	KPGCADACVIMPNENQSI	RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGFLDP	120
Db	61	KPGCADACVIMPNENQSI	RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGFLDP	120

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QY      121 TAAIVSSDTTA 131
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Db      121 TAAIVSSDTTA 131

RESULT 2
US-10-244-065-80
; Sequence 80, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; TITLE OF INVENTION: Method of Preparation and Use
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-244-065-80

Query Match      100.0%; Score 668; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MANKPMQPIITSTANKIVMSDPTLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY      61 KPEGCADACVIMPENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
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      |||||
Db      121 TAAIVSSDTTA 131

RESULT 3
US-10-289-454-80
; Sequence 80, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21

QY      121 TAAIVSSDTTA 131
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Db      121 TAAIVSSDTTA 131

RESULT 4
US-10-346-190-95
; Sequence 95, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 131
; TYPE: PRT
; ORGANISM: RNA-phage AP205
US-10-346-190-95

Query Match      100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MANKPMQPIITSTANKIVMSDPTLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
      |||||
Db      1 MANKPMQPIITSTANKIVMSDPTLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY      61 KPEGCADACVIMPENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
      |||||
Db      61 KPEGCADACVIMPENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
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; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-289-454-80
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Query Match      100.0%; Score 668; DB 14; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MANKPMQPIITSTANKIVMSDPTLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
      |||||
Db      1 MANKPMQPIITSTANKIVMSDPTLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY      61 KPEGCADACVIMPENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
      |||||
Db      61 KPEGCADACVIMPENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY      121 TAAIVSSDTTA 131
      |||||
Db      121 TAAIVSSDTTA 131
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RESULT 4
US-10-346-190-95
; Sequence 95, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 131
; TYPE: PRT
; ORGANISM: RNA-phage AP205
US-10-346-190-95
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Query Match      100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MANKPMQPIITSTANKIVMSDPTLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
      |||||
Db      1 MANKPMQPIITSTANKIVMSDPTLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY      61 KPEGCADACVIMPENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
      |||||
Db      61 KPEGCADACVIMPENQSI RTVSSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
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QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 5
US-10-465-811-90
; Sequence 90, Application US/10465811
; Publication No. US2004005338A1
; GENERAL INFORMATION:
; APPLICANT: BACHMANN, MARTIN F
; APPLICANT: RENNER, WOLFGANG A
; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS:
; FILE REFERENCE: 1700.0290004
; CURRENT APPLICATION NUMBER: US/10/465,811
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/389,898
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-465-811-90

Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKPMQPIITSTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 6
US-10-289-456-112
; Sequence 112, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 112
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
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US-10-289-456-112

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Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKPMQPIITSTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
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RESULT 7

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US-10-622-064-14
; Sequence 14, Application US/10622064
; Publication No. US20040059094A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Maurer, Patrick F
; TITLE OF INVENTION: Hapten-Carrier Conjugates and Uses Thereof
; FILE REFERENCE: 1700.0300001
; CURRENT APPLICATION NUMBER: US/10/622,064
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,575
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-064-14
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Query Match 100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKPMQPIITSTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVYKRPAP 60

QY 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

QY 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
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RESULT 8

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US-10-617-876-1
; Sequence 1, Application US/10617876
; Publication No. US20040076611A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tisseot, Alain
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Molecular Antigen Arrays
; FILE REFERENCE: 1700.0310001
; CURRENT APPLICATION NUMBER: US/10/617,876
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/396,126
; PRIOR FILING DATE: 2002-07-17
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; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-617-876-1

Query Match      100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQKRVKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQKRVKVGIAELNNVSGQYVSVYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 9
US-10-622-124-28
; Sequence 28, Application US/10622124
; Publication No. US20040076645A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulurija, Alma
; TITLE OF INVENTION: Chrelin-Carrier Conjugates
; FILE REFERENCE: 1700.0340001
; CURRENT APPLICATION NUMBER: US/10/622,124
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,638
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-124-28

Query Match      100.0%; Score 668; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQKRVKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQKRVKVGIAELNNVSGQYVSVYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 10
US-10-622-087-28
; Sequence 28, Application US/10622087
; Publication No. US20040141984A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Tissot, Alain
; APPLICANT: Ortman, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
```

```
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Amyloid Beta 1-6 Antigen Arrays
; FILE REFERENCE: 1700.0350002
; CURRENT APPLICATION NUMBER: US/10/622,087
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,639
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/470,432
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Bacteriophage AP205
US-10-622-087-28

Query Match      100.0%; Score 668; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 7.9e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQKRVKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQKRVKVGIAELNNVSGQYVSVYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131

RESULT 11
US-10-243-739-81
; Sequence 81, Application US/10243739
; Publication No. US20030091593A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: In vivo Activation of Antigen Presenting Cells for Enhancement of
; TITLE OF INVENTION: Immune Responses Induced by Virus Like Particles
; FILE REFERENCE: 1700.0210001
; CURRENT APPLICATION NUMBER: US/10/243,739
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/318,967
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-243-739-81

Query Match      98.8%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQKRVKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQKRVKVGIAELNNVSGQYVSVYKRPAP 60

Qy 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIQRTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120

Qy 121 TAAIVSSDTTA 131
Db 121 TAAIVSSDTTA 131
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```
Db      121 TAAIVSSDTTA 131

RESULT 12
US-10-244-065-81
; Sequence 81, Application US/10244065
; Publication No. US20030099668A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F.
; APPLICANT: Storni, Tazio
; APPLICANT: Maurer, Patrick
; APPLICANT: Tissot, Alain
; APPLICANT: Schwarz, Katrin
; APPLICANT: Meijerink, Edwin
; APPLICANT: Lipowsky, Gerard
; APPLICANT: Pumps, Paul
; APPLICANT: Cielens, Indulis
; APPLICANT: Renhofa, Regina
; TITLE OF INVENTION: Packaging of Immunostimulatory Substances into Virus-like Particles
; FILE REFERENCE: 1700.0220001
; CURRENT APPLICATION NUMBER: US/10/244,065
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/374,145
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/318,994
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-244-065-81

Query Match      98.8%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
Db      1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
QY      61 KPEGCADACVIMPENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db      61 KPEGCADACVIMPENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
QY      121 TAAIVSSDTTA 131
Db      121 TAAIVSSDTTA 131

RESULT 13
US-10-289-454-81
; Sequence 81, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
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; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP205 coat protein
US-10-289-454-81

Query Match      98.8%; Score 660; DB 14; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
Db      1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
QY      61 KPEGCADACVIMPENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db      61 KPEGCADACVIMPENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
QY      121 TAAIVSSDTTA 131
Db      121 TAAIVSSDTTA 131

RESULT 14
US-10-346-190-96
; Sequence 96, Application US/10346190
; Publication No. US20030219459A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Pelliccioli, Erica
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Prion Protein Carrier-Conjugates
; FILE REFERENCE: 1700.0290003
; CURRENT APPLICATION NUMBER: US/10/346,190
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/396,590
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/393,725
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 60/389,898
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 10/050,902
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 131
; TYPE: PRT
; ORGANISM: RNA-phage AP205
US-10-346-190-96

Query Match      98.8%; Score 660; DB 15; Length 131;
Best Local Similarity 99.2%; Pred. No. 7e-70;
Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
Db      1 MANKTQPIITSTANKIWSDPTRLSTTFSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
QY      61 KPEGCADACVIMPENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
Db      61 KPEGCADACVIMPENQSIPTVSGSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
QY      121 TAAIVSSDTTA 131
Db      121 TAAIVSSDTTA 131
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Db 121 TAAIVSSDTTA 131

RESULT 15
 US-10-465-811-93
 ; Sequence 93, Application US/10465811
 ; Publication No. US20040005338A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BACHMANN, MARTIN F
 ; APPLICANT: RENNER, WOLFGANG A
 ; TITLE OF INVENTION: PACKAGED VIRUS-LIKE PARTICLES FOR USE AS ADJUVANTS.
 ; FILE OF INVENTION: METHOD OF PREPARATION AND USE
 ; FILE REFERENCE: 1700.0290004
 ; CURRENT APPLICATION NUMBER: US/10/465,811
 ; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: US 60/389,898
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 93
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Bacteriophage AP205 mutant
 US-10-465-811-93

Query Match 98.8%; Score 660; DB 15; Length 131;
 Best Local Similarity 99.2%; Pred. No. 7e-70; Mismatches 1; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKPMOPITSTANKIIVMSDPTLSTTFSSALLRQVRKVGIAELNNVSGQYVSVKRPAP 60
 Db |||||
 QY 1 MANKPMOPITSTANKIIVMSDPTLSTTFSSALLRQVRKVGIAELNNVSGQYVSVKRPAP 60
 Db |||||
 QY 61 KPEGCADACVIMPENQSIPTVIGSNAENLATLKAWEETHKRNVDTLFASGNAGLGFLDP 120
 Db |||||
 QY 61 KPEGCADACVIMPENQSIPTVIGSNAENLATLKAWEETHKRNVDTLFASGNAGLGFLDP 120
 Db |||||
 QY 121 TAAIVSSDTTA 131
 Db |||||
 QY 121 TAAIVSSDTTA 131

Search completed: June 1, 2005, 09:50:59
 Job time : 92 secs

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QM protein - protein search, using sw model

Run on: June 1, 2005, 09:35:42 ; Search time 30 Seconds
(without alignments)
325.968 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668

Sequence: 1 MANKPMPQITSTANKIWS.....NAGLGFLDPTAIVSSDTTA 131

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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- 6: /cgn2_6/ptodata/1/iaa/backfilee1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	11.8	332	4	US-09-313-942-10
2	79	11.8	488	2	US-08-599-455B-5
3	79	11.8	488	3	US-09-069-781B-5
4	79	11.8	488	3	US-09-137-132-5
5	79	11.8	488	3	US-08-864-564A-5
6	79	11.8	488	4	US-09-094-410-5
7	79	11.8	488	4	US-08-708-123D-5
8	79	11.8	488	4	US-08-583-153A-5
9	79	11.8	488	4	US-08-638-524B-5
10	79	11.8	658	2	US-08-825-558-4
11	79	11.8	658	3	US-09-312-611-4
12	79	11.8	708	1	US-07-797-556-2
13	79	11.8	708	1	US-08-308-881-2
14	79	11.8	708	2	US-09-058-263-2
15	79	11.8	708	2	US-09-059-099-2
16	79	11.8	708	3	US-09-058-264-2
17	79	11.8	708	4	US-09-455-962-2
18	79	11.8	708	5	PCT-US95-06530-2
19	79	11.8	859	4	US-09-313-942-7
20	79	11.8	918	2	US-08-825-558-6
21	79	11.8	918	3	US-09-312-611-6
22	79	11.8	918	3	US-09-853-180B-3
23	79	11.8	951	4	US-09-313-942-9
24	79	11.8	1158	4	US-09-313-942-26
25	79	11.8	1168	4	US-09-313-942-24
26	73	10.9	488	4	US-09-252-991A-28535
27	72	10.8	185	4	US-09-252-991A-31599

28	70.5	10.6	248	4	US-09-252-991A-20247	Sequence 20247, A
29	70.5	10.6	5087	3	US-09-144-085-1	Sequence 1, Appli
30	70.5	10.6	6095	3	US-09-144-085-2	Sequence 2, Appli
31	70	10.5	179	4	US-09-270-767-43725	Sequence 43725, A
32	70	10.5	520	4	US-09-461-325-144	Sequence 144, App
33	70	10.5	520	4	US-10-012-542-144	Sequence 144, App
34	70	10.5	520	4	US-10-115-123-144	Sequence 144, App
35	69	10.3	414	4	US-09-489-039A-13320	Sequence 13320, A
36	69	10.3	694	4	US-09-328-352-7276	Sequence 7276, A
37	67.5	10.1	300	4	US-09-252-991A-19422	Sequence 19422, A
38	67.5	10.1	343	3	US-08-858-003-32	Sequence 32, Appli
39	67.5	10.1	343	3	US-09-078-166-32	Sequence 32, Appli
40	67.5	10.1	343	3	US-08-997-467-32	Sequence 32, Appli
41	67	10.0	701	4	US-09-538-092-303	Sequence 303, App
42	67	10.0	707	4	US-09-021-560-4	Sequence 4, Appli
43	67	10.0	707	4	US-09-202-178A-4	Sequence 4, Appli
44	66.5	10.0	480	4	US-09-710-279-2852	Sequence 2852, Ap
45	66.5	10.0	480	4	US-09-710-279-2986	Sequence 2986, Ap

ALIGNMENTS

RESULT 1

US-09-313-942-10

; Sequence 10, Application US/09313942

; Patent No. 6472179

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

; TITLE OF INVENTION: AND USING

; FILE REFERENCE: REG 203-A

; CURRENT APPLICATION NUMBER: US/09/313,942

; CURRENT FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: 09/313,942

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: 60/101,858

; PRIOR FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 332

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-313-942-10

Query Match 11.8%; Score 79; DB 4; Length 332;

Best Local Similarity 25.5%; Pred. No. 0.36;

Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIYMSDPTRLSTTFSASLLR-ORVKVGIAELNNVSGQYVYKRPAPKPEGCAD 67

Db 82 INRTASSVFTDIFASLIQTCNLTGQLEQNVYGIITSG-----LPPEKPKQL-- 132

QY 68 ACVIMENQSTRTVISGSAENLA-----TLKAEWETHK 101

Db 133 SCIV--NEGKORCEWDGGRGTHLETNFTLKSEWATHK 168

RESULT 2

US-08-599-455B-5

; Sequence 5, Application US/08599455B

; Patent No. 5972621

; GENERAL INFORMATION:

; APPLICANT: Tartaglia, Louis A.

; APPLICANT: Tepper, Robert I.

; APPLICANT: Culpepper, Janice A.

; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT

; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

```
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-599-455B-5

Query Match 11.8%; Score 79; DB 2; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWMSPDTRLSSTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPECCAD 67
Db 53 INRTASSVTFTDIASLNILQTCNLTGQLEQNVYGITISG-----LPPEKPKNL-- 103
Qy 68 ACVIMPNENQSIPTVISGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCEWDGGRHLETNFTLKSEWATHK 139

RESULT 3
US-09-069-781B-5
; Sequence 5, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-781B-5

Query Match 11.8%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIWMSPDTRLSSTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPECCAD 67
Db 53 INRTASSVTFTDIASLNILQTCNLTGQLEQNVYGITISG-----LPPEKPKNL-- 103
Qy 68 ACVIMPNENQSIPTVISGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKKMRCEWDGGRHLETNFTLKSEWATHK 139

RESULT 4
US-09-137-132-5
; Sequence 5, Application US/09137132
; Patent No. 6380363
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
```

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; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-137-132--5

Query Match 11.8%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVMSDPTRLSTTFSALLR-QRVKVGIAELNNVSGQVSVYKRPAPKPGCAD 67
Db 53 INRTASSVTFTDIASLNILQTCNLTGQEQNVYGITIISG-----LPPEKPKNL-- 103

QY 68 ACVIMNENQSIPTVSGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKQRCWDGGRETHLETNFTLKSEWATHK 139

RESULT 5
US-08-864-564A-5
; Sequence 5, Application US/08864564A
; Patent No. 6395498
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.

; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-137-132--5

Query Match 11.8%; Score 79; DB 3; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

QY 9 ITSTANKIVMSDPTRLSTTFSALLR-QRVKVGIAELNNVSGQVSVYKRPAPKPGCAD 67
Db 53 INRTASSVTFTDIASLNILQTCNLTGQEQNVYGITIISG-----LPPEKPKNL-- 103

QY 68 ACVIMNENQSIPTVSGSAENLA-----TLKAEWETHK 101
Db 104 SCIV--NEGKQRCWDGGRETHLETNFTLKSEWATHK 139

RESULT 6
US-09-094-410-5
; Sequence 5, Application US/09094410
; Patent No. 6403552
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
```


CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,153A
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/016001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-583-153A-5

Query Match 11.8%; Score 79; DB 4; Length 488;
Best Local Similarity 25.5%; Pred. No. 0.64; Mismatches 21; Indels 16; Gaps 5;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTAKIVMSDPTRLSTTFSSALLR-QRVKVGIAELNNVSGQVSVYKRPAPKPGCAD 67
Db 53 INRTASSVTFDASLNQLTLCNLTGQLEQNVYGIITSG-----LPPEKPKNL-- 103

Qy 68 ACVMPNENSIQRTVSGSAENLA---TLKAEWETHK 101
Db 104 SCIV--NEGKVMRCWDGGRETHLETFTLKSEWATHK 139

RESULT 9
US-08-638-524B-5
Sequence 5, Application US/08638524B
Patent No. 6548269
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB
TITLE OF INVENTION: CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

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; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-825-558-4

Query Match 11.8%; Score 79; DB 2; Length 658;
Best Local Similarity 25.5%; Pred. No. 1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVMSDPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITISG-----LPPEKPKNL-- 132
Qy 68 ACVIMPNENOSIRTVISSAENLA-----TLKAETHK 101
Db 133 SCIV--NEGKMRCEWDGGREHLETFNFTLKSEWATHK 168

RESULT 11
US-09-312-611-4
; Sequence 4, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-312-611-4

Query Match 11.8%; Score 79; DB 3; Length 658;
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Best Local Similarity 25.5%; Pred. No. 1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVMSDPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITISG-----LPPEKPKNL-- 132
Qy 68 ACVIMPNENOSIRTVISSAENLA-----TLKAETHK 101
Db 133 SCIV--NEGKMRCEWDGGREHLETFNFTLKSEWATHK 168

RESULT 12
US-07-797-556-2
; Sequence 2, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-797-556-2

Query Match 11.8%; Score 79; DB 1; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;

Qy 9 ITSTANKIVMSDPTRLSTTFSASLLR-QRVKVGIAELNNVSGQVSVYKRPAPKPEGCAD 67
Db 82 INRTASSVTFTDIASLNQITCNILTFGQLEQNVYGITISG-----LPPEKPKNL-- 132
Qy 68 ACVIMPNENOSIRTVISSAENLA-----TLKAETHK 101
Db 133 SCIV--NEGKMRCEWDGGREHLETFNFTLKSEWATHK 168

RESULT 13
US-08-308-881-2
; Sequence 2, Application US/08308881
; Patent No. 5783672
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-059-099-2
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Query Match 11.8%; Score 79; DB 2; Length 708;
Best Local Similarity 25.5%; Pred. No. 1.1;
Matches 25; Conservative 21; Mismatches 36; Indels 16; Gaps 5;
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QY 9 ITSTANKIVMSDPTRLSTTFESALLR-QRVKVGIAELNNVSGQYVSVYKRPAPKPEGCAD 67
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Db 82 INETASSVTFTDIASLNIQLTCNLTFGQLEQNVYGITIISG-----LPPEKPKNL-- 132
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QY 68 ACVIMPENQSIQRTVISGSAENLA----TLKAEWETHK 101
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Db 133 SCIV--NEGKKMRCEWDGGRETHLETNFTLKSEWATHK 168
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Search completed: June 1, 2005, 09:47:52
Job time : 32 secs
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OM protein - protein search, using sw model

Run on: June 1, 2005, 09:31:22; Search time 114 Seconds
(without alignments)
444.435 Million cell updates/sec

Title: US-10-617-876-1

Perfect score: 668

Sequence: 1 MANKPQPTSTANKIWSG.....NAGLGFLDPTAIVSSDTTA 131

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	668	100.0	131	6	ABR56508 AP205 coa
2	668	100.0	131	6	ABU09694 Bacteriop
3	668	100.0	131	6	ABR44611 AP205 coa
4	668	100.0	131	7	ADD24202 Bacteriop
5	668	100.0	131	7	ADJ82145 Protein f
6	668	100.0	131	7	ADK17201 API prote
7	668	100.0	131	8	ADJ36389 Bacteriop
8	668	100.0	131	8	ADI40710 Bacteriop
9	668	100.0	131	8	ADJ67170 Bacteriop
10	668	100.0	131	8	ADK52204 Bacteriop
11	668	100.0	131	8	ADL98301 Bacteriop
12	660	98.8	131	6	ABR56509 AP205 coa
13	660	98.8	131	6	ABU09695 Bacteriop
14	660	98.8	131	6	ABR44612 AP205 coa
15	660	98.8	131	7	ADD24203 Bacteriop
16	660	98.8	131	7	ADJ82146 Protein f
17	660	98.8	131	7	ADK17202 AP3 prote
18	660	98.8	131	8	ADJ36392 Bacteriop
19	660	98.8	131	8	ADI40712 Bacteriop
20	660	98.8	131	8	ADJ67171 Bacteriop
21	660	98.8	131	8	ADK52205 Bacteriop
22	660	98.8	131	8	ADL98305 Mutant Ba
23	80	12.0	194	5	ABU05510 M. tuberc
24	79	11.8	329	2	AAW17859 Rheumatol
25	79	11.8	329	8	ADR14425 Human NF-

ALIGNMENTS

RESULT 1

ABR56508

ID ABR56508 standard; protein; 131 AA.

XX ABR56508;

XX AC

XX XX

DT 28-JUL-2003 (first entry)

XX XX

DE AP205 coat protein SEQ ID NO:80.

XX XX

KW Antigen presenting cell; APC; immune response; virus like particle; VLP;

KW Cytostatic; virucide; antibacterial; antiparasitic; fungicide;

KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;

KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;

KW antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;

KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;

KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;

KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;

KW inflammatory autoimmune disease.

XX XX

OS Synthetic.

XX XX

PN WO2003024480-A2.

XX XX

PD 27-MAR-2003.

XX XX

PF 16-SEP-2002; 2002WO-IB004252.

XX XX

PR 14-SEP-2001; 2001US-0318967P.

XX XX

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX XX

PI Bachmann MF, Storni T, Lechner F;

XX XX

DR WPI; 2003-363095/34.

XX XX

PT A composition, useful for enhancing an immune response against an antigen

or a virus-like particle, enhancing anti-viral protection in an animal,

or immunizing or treating tumors or infectious diseases, e.g. viral

infections.

XX XX

PS Disclosure; Page 239-240; 243pp; English.

XX XX

CC The present invention describes a composition (C) for enhancing an immune

response against an antigen or a virus-like particle in an animal. (C)

comprise a virus-like particle (VLP) bound to at least one antigen, or a

VLP capable of being recognised by the immune system of the animal. Also

described: (1) enhancing an immune response against an antigen or a VLP

CC

CC

CC

CC

PA (SCHW/) SCHWARZ K.
 PA (MEIJ/) MEIJERINK E.
 PA (LIPO/) LIPOWSKY G.
 PA (PUMP/) PUMPENS P.
 PA (CIEL/) CIELENS I.
 PA (RENH/) RENHOFA R.
 XX
 PI Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;
 PI Pumpens P, Cielems I, Renhofs R, Bachmann MF, Storni T;
 XX
 DR WPI; 2003-354564/33.
 XX
 PT New compositions comprising immunostimulatory substances packaged into
 PT virus-like particles, useful as a vaccine for enhancing an immune
 PT response in animals, e.g. for treating or preventing allergies, tumors or
 PT viral infections.
 XX
 PS Disclosure; Page 319; 323pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response in an animal. (C) comprises a virus-like particle (VLP), and an
 CC immunostimulatory substance. The immunostimulatory substance is bound to
 CC the VLP. Also described: (1) enhancing an immune response in an animal by
 CC introducing (C) into the animal; (2) producing (C) for enhancing an
 CC immune response in an animal; (3) vaccines comprising (C) together with a
 CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
 CC treating an animal by: (a) administering the vaccine to the animal; (b)
 CC priming a T cell response in the animal by administering the vaccine; or
 CC (c) boosting a T cell response in the animal by administering the
 CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (1) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 131 AA;

Query Match 100.0%; Score 668; DB 6; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQKVKVIGIAELNNVSGQYVSVYKRPAP 60
 DB 1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQKVKVIGIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIQRTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
 DB 61 KPEGCADACVIMPNENQSIQRTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131

RESULT 4
 ID ADD24202 standard; protein; 131 AA.
 XX
 AC ADD24202;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Bacteriophage AP205 coat protein #1.
 XX
 KW vaccine composition; virus-like particle; core particle;

KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion; AP205; coat protein.
 OS Bacteriophage AP205.
 XX
 PN WO2003059386-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-EP000460.
 XX
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 XX WPI; 2003-598483/56.
 DR N-PSDB; ADD24201.
 XX
 PT A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phase) and at least one prion protein or peptide bound to the virus-like
 PT particle.
 XX
 PS Disclosure; SEQ ID NO 95; 246pp; English.
 XX
 CC This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a RNA-phase AP205 coat protein
 CC which is related to the invention.
 XX
 SQ Sequence 131 AA;

Query Match 100.0%; Score 668; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQKVKVIGIAELNNVSGQYVSVYKRPAP 60
 DB 1 MANKMPQITSTANKIWSDPTRLSTTFSASLLRQKVKVIGIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIQRTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
 DB 61 KPEGCADACVIMPNENQSIQRTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
 QY 121 TAAIVSSDTTA 131
 DB 121 TAAIVSSDTTA 131

RESULT 5
 ID ADJ82145 standard; protein; 131 AA.
 XX
 AC ADJ82145;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Protein for RANKL antigen array to treat bone disease.
 XX

KW osteopathic; vaccine; core particle; antigenic determinant; RANKL;
 KW bone disease; encephalopathy; immune system stimulation.
 XX Unidentified.
 XX WO2003039225-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-EP012449.
 XX
 XX 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396635P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX Bachmann M, Maurer P, Spohn G;
 XX WPI; 2003-441430/41.
 XX
 XX New compositions comprising a core particle and at least one antigen or
 PT antigenic determinant, useful for as a vaccine for therapy or prophylaxis
 PT of bone diseases, particularly mammalian encephalopathies.
 XX
 XX Disclosure; SEQ ID NO 112; 222pp; English.
 XX
 XX The invention relates to a composition comprising a core particle having
 CC at least one first attachment site, and at least one antigen or antigenic
 CC determinant having at least one second attachment site. The antigen or
 CC antigenic determinant is a RANKL protein, RANKL fragment or RANKL
 CC peptide. The second attachment site is (non-) naturally occurring with
 CC the antigen or antigenic determinant, and is capable of association to
 CC the first attachment site. The antigen or antigenic determinant and the
 CC core particle interact through the association to form an ordered and
 CC repetitive antigen array. The composition is useful as a medicament, or
 CC for the manufacture of a medicament for treating bone diseases. The
 CC composition is especially useful for as a vaccine for therapy or
 CC prophylaxis of bone diseases, particularly mammalian encephalopathies,
 CC and for stimulating mammalian immune system. This sequence represents a
 CC protein of the invention.
 XX
 XX Sequence 131 AA;

Query Match 100.0%; Score 668; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPMQPTITSTANKIIVNSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
 Db 1 MANKPMQPTITSTANKIIVNSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDITLFAAGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDITLFAAGNAGLGLDLP 120
 QY 121 TAAIVSSDITTA 131
 Db 121 TAAIVSSDITTA 131

RESULT 6
 ADK17201
 ID ADK17201 standard; protein; 131 AA.
 XX
 XX AC ADK17201;
 XX
 XX DT 06-MAY-2004 (first entry)
 XX
 XX DE API protein for repetitive antigen array.
 XX
 XX KW antiallergic; antiasthmatic; cytostatic; vaccine; virus-like particle;

KW interleukin; IL-5; IL-13; eotaxin; repetitive antigen array;
 KW allergic eosinophilic disease; asthma; Hodgkin's lymphoma.
 XX Unidentified.
 XX WO2003040164-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 07-NOV-2002; 2002WO-EP012455.
 XX
 XX 07-NOV-2001; 2001US-0331045P.
 PR 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 19-JUL-2002; 2002US-0396636P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX Bachmann M, Jennings G, Sonderegger I;
 XX WPI; 2003-441518/41.
 XX
 XX Composition comprising an ordered and repetitive antigen or antigenic
 PT determinant array, useful as a medicament, or for manufacturing a
 PT medicament for treating allergic eosinophilic diseases, e.g. asthma, or
 PT Hodgkin's lymphoma.
 XX
 XX Disclosure; SEQ ID NO 80; 245pp; English.
 XX
 XX The invention relates to a composition comprising a virus-like particle
 CC and at least one antigen, which is a protein or peptide of interleukin
 CC (IL)-5, IL-13 or eotaxin and is bound to the virus-like particle, or a
 CC core particle with at least one first attachment site and at least one
 CC antigen with at least one second attachment site, where the antigen is a
 CC protein or peptide of IL-5, IL-13 or eotaxin. The second attachment site
 CC is an attachment site naturally or not naturally occurring with the
 CC antigen or antigenic determinant. The second attachment site is capable
 CC of association to the first attachment site, and where the antigen or
 CC antigenic determinant and the core particle interact through the
 CC association to form an ordered and repetitive antigen array. The
 CC compositions are useful as medicaments, or for manufacturing a medicament
 CC or a vaccine for treating allergic eosinophilic diseases, e.g. asthma, or
 CC Hodgkin's lymphoma and related diseases. This sequence is used to
 CC generate the compound of the invention.
 XX
 XX Sequence 131 AA;

Query Match 100.0%; Score 668; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPMQPTITSTANKIIVNSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
 Db 1 MANKPMQPTITSTANKIIVNSDPTRLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDITLFAAGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDITLFAAGNAGLGLDLP 120
 QY 121 TAAIVSSDITTA 131
 Db 121 TAAIVSSDITTA 131

RESULT 7
 ADJ36389
 ID ADJ36389 standard; protein; 131 AA.
 XX
 XX AC ADJ36389;
 XX
 XX DT 22-APR-2004 (first entry)
 XX
 XX DE Bacteriophage AP205 coat protein virus-like particle.

XX antiallergic; cytostatic; virucide; immunostimulant; vaccine;
 KW immune response; virus-like particle; immunostimulatory; allergy; tumour;
 KW chronic disease; chronic viral disease; bacteriophage AP205;
 KW coat protein; VLP; adjuvant.
 XX Bacteriophage AP205.
 OS
 XX
 PN WO2004000351-A1.
 XX
 PD 31-DEC-2003.
 XX
 XX 20-JUN-2003; 2003WO-EP006541.
 PF
 XX 20-JUN-2002; 2002US-0389898P.
 PR
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA Bachman MF, Renner WA;
 XX
 PI Bachman MF, Renner WA;
 XX
 XX WPI; 2004-108361/11.
 DR
 XX New compositions comprising a virus-like particle (VLP), an
 XX immunostimulatory substance bound to the VLP, and an antigen mixed with
 PT the VLP, useful for enhancing immune response or for treating e.g. tumors
 PT or chronic viral diseases.
 PT
 XX Example 16; SEQ ID NO 90; 252pp; English.
 PS
 XX The invention describes a composition for enhancing an immune response in
 XX an animal comprising a virus-like particle, an immunostimulatory
 CC substance bound to the virus-like particle, and an antigen mixed with the
 CC virus-like particle. The composition or the vaccine is useful in the
 CC manufacture of a pharmaceutical for the treatment of a disorder or
 CC disease such as allergies, tumours, chronic diseases and chronic viral
 CC diseases. The composition is also useful for enhancing an immune response
 CC in an animal. This is the amino acid sequence of a bacteriophage AP205
 CC coat protein a virus like particle (VLP) that can be used in the adjuvant
 CC of the invention.
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPQPTITSTANKIWSDPTRLSTTFSSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
 Db 1 MANKPQPTITSTANKIWSDPTRLSTTFSSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
 QY 61 KPEGCADACVIMPENQSI RTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPENQSI RTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131
 RESULT 8
 ADI40710
 ID ADI40710 standard; protein; 131 AA.
 XX
 AC ADI40710;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Bacteriophage AP205 coat protein SEQ ID NO:1.
 XX virus-like particle; bacteriophage AP205; coat protein; cytostatic;
 KW vaccine; gene therapy; cancer; allergy; asthma.
 KW
 OS Bacteriophage AP205.

XX WO2004007538-A2.
 XX
 PD 22-JAN-2004.
 XX
 PF 14-JUL-2003; 2003WO-EP007572.
 XX
 PR 17-JUL-2002; 2002US-0396126P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 PI Bachmann MF, Tissot A, Pumpens P, Cielens I, Renhofs R;
 XX
 DR WPI; 2004-122882/12.
 DR N-PSDB; ADI40711.
 XX
 XX New virus-like particle, useful for preparing a composition for treating
 PT or preventing a disease e.g., cancer, allergy or asthma.
 PT
 XX Claim 1; SEQ ID NO 1; 170pp; English.
 PS
 XX The present invention describes a virus-like particle (I) which
 CC comprises: (a) a protein having the 131-amino acid sequence of
 CC bacteriophage AP205 coat protein or the mutant coat protein, see ADI40710
 CC or ADI40712 respectively; or (b) a mutein of the protein of (a). Also
 CC described: (1) a mutein of the recombinant protein having the 131-amino
 CC acid sequence; (2) a vector for producing a AP205 virus like particle
 CC comprising a nucleotide sequence being at least 80, 90, 95 or 99%
 CC identical to that of the sequence comprising 3635 or 3613 bp or producing
 CC a recombinant protein comprising a nucleotide sequence encoding a
 CC polypeptide fused to a protein; (3) a pharmaceutical composition
 CC comprising the composition and a carrier; (4) a process for producing a
 CC non-naturally occurring, ordered and repetitive antigen array; (5) a
 CC method of treating or preventing a disease, disorder or physiologic
 CC conditions in an individual; (6) a nucleic acid molecule comprising 3635-
 CC bp sequence; (7) a host cell containing a nucleic acid or a vector; and
 CC (8) a method of producing the virus-like particle. (I) has cytostatic
 CC activity, and can be used in vaccines, and in gene therapy. The virus-
 CC like particle is useful for preparing a composition for treating or
 CC preventing a disease e.g., cancer, allergy or asthma. The present
 CC sequence represents the bacteriophage AP205 coat protein, which is used
 CC in the exemplification of the present invention.
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPQPTITSTANKIWSDPTRLSTTFSSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
 Db 1 MANKPQPTITSTANKIWSDPTRLSTTFSSASLLRQKVKGIAELNNVSGQYVSVKRPAP 60
 QY 61 KPEGCADACVIMPENQSI RTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPENQSI RTVIGSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131
 RESULT 9
 ADJ67170
 ID ADJ67170 standard; protein; 131 AA.
 XX
 AC ADJ67170;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Bacteriophage AP205 coat protein for antigen display array.
 XX anorectic; core particle; antigenic determinant; ghrelin; P-pilin;
 KW

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KW antigenic array.
XX Bacteriophage AP205.
OS WO2004009124-A2.
PN 29-JAN-2004.
XX 18-JUL-2003; 2003WO-EP007849.
XX 19-JUL-2002; 2002US-0396638P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX Bachmann MF, Fulurija A;
XX WPI; 2004-132866/13.
XX New composition comprising a core particle having a first attachment site
XX and an antigen or antigenic determinant which is a ghrelin or ghrelin
XX peptide having a second attachment site, useful for treating obesity.
XX Claim 12; SEQ ID NO 28; 175pp; English.
XX The invention relates to a new composition comprising: (i) a core
XX particle with at least one first attachment site; and (ii) at least one
XX antigen or antigenic determinant with at least one second attachment
XX site, where the antigen or antigenic determinant is ghrelin or a ghrelin
XX peptide, and where the second attachment site being consisting of an
XX attachment site not naturally occurring with the antigen or antigenic
XX determinant and an attachment site naturally occurring with the antigen
XX or antigenic determinant, where the second attachment site is capable of
XX association to the first attachment site, and where the ghrelin or a
XX ghrelin peptide and the core particle interact through the association to
XX form an ordered and repetitive antigen array. The composition is useful
XX for treating obesity. The repetitive array may form part of a phage or
XX bacterial display array. This peptide corresponds to a Bacteriophage
XX AP205 coat protein which can be used as part of the repetitive or antigenic
XX array.
XX SQ Sequence 131 AA;
Query Match 100.0%; Score 668; DB 8; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Qy 61 KPEGCADACVIMPNENQSIIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGLDLP 120
Qy 121 TAAIVSSDDTTA 131
Db 121 TAAIVSSDDTTA 131
RESULT 10
ADK52204
ID ADK52204 standard; protein; 131 AA.
XX AC ADK52204;
XX 20-MAY-2004 (first entry)
XX Bacteriophage AP205 coat protein.
XX neuroprotective; nootropic; vaccine; amyloid beta 1-6 peptide;
KW core particle; antigen array; Alzheimer's disease; RNA Bacteriophage;
KW coat protein.
XX

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```

OS Bacteriophage AP205.
XX WO2004016282-A1.
XX 26-FEB-2004.
XX 18-JUL-2003; 2003WO-EP007864.
XX 19-JUL-2002; 2002US-0396639P.
XX 15-MAY-2003; 2003US-0470432P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX (NOVS ) NOVARTIS PHARMA AG.
XX Bachmann MF, Tissot A, Ortman R, Lueoend R, Staufenbiel M;
XX Frey P;
XX WPI; 2004-203731/19.
XX Composition comprising a core particle with at least one attachment site,
XX and an antigenic amyloid beta 1-6 peptide, useful for treating diseases
XX such as Alzheimer's disease.
XX Claim 12; SEQ ID NO 28; 184pp; English.
XX The invention describes a novel composition comprising a core particle
XX with at least one attachment site, and an antigenic amyloid beta 1-6
XX peptide. The new composition comprises: a core particle with at least one
XX first attachment site; and at least one antigen or antigenic determinant
XX with at least one second attachment site, where the antigen or antigenic
XX determinant is a Amyloid beta 1-6 peptide, and where the second
XX attachment site comprises: an attachment site not naturally occurring
XX with the antigen or antigenic determinant; or an attachment site
XX naturally occurring with the antigen or antigenic determinant. The second
XX attachment site is capable of association to the first attachment site
XX and the beta 1-6 peptide and the core particle interact through the
XX association to form an ordered and repetitive antigen array. The
XX composition is useful for the manufacture of a medicament for treating
XX Alzheimer's disease and related diseases. This is the amino acid sequence
XX of an RNA bacteriophage coat protein that can be used in the preparation
XX of the compositions and vaccines of the invention.
XX SQ Sequence 131 AA;
Query Match 100.0%; Score 668; DB 8; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Db 1 MANKPMQPIITSTANKIIVMSDPTLSTTFSASLLRQVRKVGIAELNNVSGQYVSVYKRPAP 60
Qy 61 KPEGCADACVIMPNENQSIIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGLDLP 120
Db 61 KPEGCADACVIMPNENQSIIRTVISGSAENLATLKAWEETHKRNVDTLFASGNAGLGLDLP 120
Qy 121 TAAIVSSDDTTA 131
Db 121 TAAIVSSDDTTA 131
RESULT 11
ADL98301
ID ADL98301 standard; protein; 131 AA.
XX AC ADL98301;
XX 18-NOV-2004 (first entry)
XX Bacteriophage AP205 coat protein.
XX haptan-carrier conjugate; recombinant virus protein; attachment site;
KW drug addiction; fentanyl; heroin; morphine; amphetamine; cocaine;
KW

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KW methylenedioxymethamphetamine; methamphetamine; methylphenidate;
 KW nicotine; cocaine; nornicotine; PCP; LSD; mescaline; psilocybin;
 KW tetrahydrocannabinol; diazepam; desipramine; imipramine; nortriptyline;
 KW amitriptyline; coat protein.
 XX
 OS Bacteriophage AP205.
 XX
 PN WO2004009116-A2.
 XX
 PD 29-JAN-2004.
 XX
 XX 18-JUL-2003; 2003WO-EP007850.
 XX
 XX 18-JUL-2002; 2002US-0396575P.
 PR
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX
 XX Bachmann MF, Maurer P;
 XX
 DR WPI; 2004-132865/13.
 DR N-PSDB; ADL98302.
 XX
 XX Hapten-carrier conjugate useful for treating or preventing addiction to
 PT drug, comprises core particle having first attachment site and hapten
 PT with second attachment site linked to form ordered and repetitive
 PT conjugate.
 XX
 PS Claim 14; SEQ ID NO 14; 144pp; English.
 XX
 CC The invention comprises a hapten-carrier conjugate consisting of a
 CC carrier (e.g. a recombinant virus protein) that has at least one
 CC attachment site, and at least one hapten with at least one second
 CC attachment site. The method of the invention is useful for treating or
 CC preventing addiction to a drug, such as: codeine, fentanyl, heroin,
 CC morphine, amphetamine, cocaine, methylenedioxymethamphetamine,
 CC methamphetamine, methylphenidate, nicotine, cotinine, nornicotine, PCP,
 CC LSD, mescaline, psilocybin, tetrahydrocannabinol, diazepam, desipramine,
 CC imipramine, nortriptyline and the amitriptyline class of drugs. The
 CC method of the invention is also useful for preventing and treating
 CC diseases associated with addiction. The present amino acid sequence
 CC represents a protein which is claimed for use in the hapten-carrier
 CC conjugate of the invention.
 XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 668; DB 8; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.9e-73;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVKRPAP 60
 DB 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVKRPAP 60
 QY 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
 DB 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131
 RESULT 12
 ABR56509
 ID ABR56509 standard; protein; 131 AA.
 AC ABR56509;
 XX
 XX 28-JUL-2003 (first entry)
 DT
 XX AP205 coat protein SEQ ID NO:81.
 DE
 XX Antigen presenting cell; APC; immune response; virus like particle; VLP;
 KW

KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;
 KW antiallergic; immunosuppressive; antiaddictive; antinflammatory;
 KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
 KW antihemetic; antiarthritic; vaccine; immunisation; infectious disease;
 KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 KW inflammatory autoimmune disease.
 XX
 OS Synthetic.
 XX
 PN WO2003024480-A2.
 XX
 PD 27-MAR-2003.
 XX
 XX 16-SEP-2002; 2002WO-IB004252.
 PF
 XX 14-SEP-2001; 2001US-0318967P.
 PR
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX Bachmann MF, Storni T, Lechner F;
 PI
 XX WPI; 2003-363095/34.
 DR
 XX A composition, useful for enhancing an immune response against an antigen
 PT or a virus-like particle, enhancing anti-viral protection in an animal,
 PT or immunizing or treating tumors or infectious diseases, e.g. viral
 PT infections.
 XX
 PS Disclosure; Page 240-241; 243pp; English.
 XX
 CC The present invention describes a composition (C) for enhancing an immune
 CC response against an antigen or a virus-like particle in an animal. (C)
 CC comprises a virus-like particle (VLP) bound to at least one antigen, or a
 CC VLP capable of being recognised by the immune system of the animal. Also
 CC described: (1) enhancing an immune response against an antigen or a VLP
 CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antinflammatory,
 CC antihyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antihemetic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumors and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 131 AA;
 Query Match 98.8%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 3.7e-72;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVKRPAP 60
 DB 1 MANKPMQPISTANKIWSDPTRLSTTFSASLLRQKVKVGI AELNNVSGQYVSVKRPAP 60
 QY 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
 DB 61 KPEGCADACVIMPNENQSI RTVIGSGAENLATLKAETHKRNVDTLFASGNAGLGLDP 120
 QY 121 TAAIVSSDDTTA 131
 DB 121 TAAIVSSDDTTA 131

CC antibacterial activities. (I) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence 131 AA;

Query Match 98.8%; Score 660; DB 6; Length 131;
 Best Local Similarity 99.2%; Pred. No. 3.7e-72;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKPMQPTITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQYVSVYKRPAP 60
 Db 1 MANKTQPTITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

RESULT 15
 ADD24203
 ID ADD24203 standard; protein; 131 AA.

AC ADD24203;
 DT 15-JAN-2004 (first entry)
 DE Bacteriophage AP205 coat protein #2.
 KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion; AP205; coat protein.

OS Synthetic.
 OS Bacteriophage AP205.
 PN WO2003059386-A2.
 XX 24-JUL-2003.
 XX 17-JAN-2003; 2003WO-EP000460.
 XX 18-JAN-2002; 2002US-00050902.
 XX 21-JAN-2002; 2002WO-IP000166.
 XX 08-JUL-2002; 2002US-0393725P.
 XX 18-JUL-2002; 2002US-0396590P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PI Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 DR WPI; 2003-598483/56.
 DR N-PSDB; ADD24204.
 XX A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA
 PT phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.

XX Disclosure; SEQ ID NO 96; 246pp; English.
 XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a mutant RNA-phage AP205 coat
 XX protein which is related to the invention.

XX Sequence 131 AA;
 Query Match 98.8%; Score 660; DB 7; Length 131;
 Best Local Similarity 99.2%; Pred. No. 3.7e-72;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MANKPMQPTITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQYVSVYKRPAP 60
 Db 1 MANKTQPTITSTANKIWSDPTRLSTTFSASLLRQKVGIAELNNVSGQYVSVYKRPAP 60
 QY 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 Db 61 KPEGCADACVIMPNENQSIPTVSSAENLATLKAETHKRNVDTLFASGNAGLGLDLP 120
 QY 121 TAAIVSSDTTA 131
 Db 121 TAAIVSSDTTA 131

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